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## OM protein - protein search, using sw model

Run on: June 14, 2005, 15:46:34 ; Search time 20.7308 Seconds  
(without alignments)  
50.412 Million cell updates/sec

Title: US-09-831-253F-2  
Perfect score: 89  
Sequence: 1 FCLGPCPYWISLDT 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	23	1	US-08-486-057B-26
2	89	100.0	23	2	US-08-789-588-26
3	89	100.0	25	4	US-09-095-637D-4
4	89	100.0	51	6	5168051-4
5	89	100.0	51	6	5168051-4
6	89	100.0	60	3	US-09-363-939A-122
7	89	100.0	60	4	US-09-791-301-122
8	89	100.0	70	4	US-09-848-664A-9
9	89	100.0	98	3	US-08-478-097A-1
10	89	100.0	98	3	US-08-931-858E-150
11	89	100.0	98	3	US-08-981-739-150
12	89	100.0	98	4	US-09-128-028-150
13	89	100.0	98	4	US-09-496-398-1
14	89	100.0	98	4	US-09-220-616-150
15	89	100.0	98	4	US-09-374-958C-40
16	89	100.0	98	4	US-09-220-527-150
17	89	100.0	98	4	US-09-220-407-150
18	89	100.0	112	1	US-07-979-441-1
19	89	100.0	112	1	US-08-197-792-36
20	89	100.0	112	1	US-08-486-057B-41
21	89	100.0	112	1	US-08-459-850-36
22	89	100.0	112	1	US-08-459-214-36
23	89	100.0	112	1	US-08-470-837-30
24	89	100.0	112	2	US-08-789-588-41
25	89	100.0	112	2	US-08-410-573-1
26	89	100.0	112	3	US-09-123-233-2
27	89	100.0	112	3	US-08-927-433-5

28	89	100.0	112	3	US-08-868-452-30	Sequence 30, Appl
29	89	100.0	112	4	US-09-095-637D-1	Sequence 1, Appl
30	89	100.0	112	5	PCT-US93-03068-1	Sequence 1, Appl
31	89	100.0	114	1	US-08-481-377-23	Sequence 23, Appl
32	89	100.0	114	2	US-08-491-835-21	Sequence 21, Appl
33	89	100.0	114	3	US-09-153-733A-23	Sequence 23, Appl
34	89	100.0	114	3	US-08-946-092A-21	Sequence 21, Appl
35	89	100.0	114	3	US-09-172-062-21	Sequence 21, Appl
36	89	100.0	114	3	US-08-624-635-22	Sequence 22, Appl
37	89	100.0	114	3	US-09-301-520D-21	Sequence 21, Appl
38	89	100.0	114	3	US-09-389-705-23	Sequence 23, Appl
39	89	100.0	114	5	PCT-US94-00666-23	Sequence 23, Appl
40	89	100.0	114	5	PCT-US94-00685-21	Sequence 21, Appl
41	89	100.0	115	1	US-08-581-529B-19	Sequence 19, Appl
42	89	100.0	115	1	US-08-455-559-25	Sequence 25, Appl
43	89	100.0	115	2	US-08-525-596B-29	Sequence 29, Appl
44	89	100.0	115	2	US-08-581-528A-19	Sequence 19, Appl
45	89	100.0	115	3	US-09-097-616-19	Sequence 19, Appl

## ALIGNMENTS

RESULT 1  
US-08-486-057B-26  
Sequence 26, Application US/08486057B  
Patent No. 5650494  
GENERAL INFORMATION:  
APPLICANT: Cerletti, Nico  
APPLICANT: McMaster, Gary K.  
APPLICANT: Cox, David  
APPLICANT: Schmitz, Albert  
APPLICANT: Meyhack, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Henry P. No. 5650494k  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,057B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/201,703  
FILING DATE: 25-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,309  
FILING DATE: 13-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/621,502  
FILING DATE: 03-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8927546.5  
FILING DATE: 06-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5650494k, Henry P.  
REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 4-17861/\*Cont3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-486-057B-26

Query Match 100.0%; Score 89; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2,1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14  
| | | | | | | | | | | | | | | | | | | | | |  
Db 6 FCLGPCPYIWSLDT 19

RESULT 2  
US-08-789-588-26  
Sequence 26, Application US/08789588  
Patent No. 5922846  
GENERAL INFORMATION:  
APPLICANT: Cerletti, Nico  
APPLICANT: McMaster, Gary K.  
APPLICANT: Cox, David  
APPLICANT: Schmitz, Albert  
APPLICANT: Mayhock, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly  
TITLE OF INVENTION: Produced TGF-beta-like Proteins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Henry P. No. 5922846ak  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/789,588  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,057  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/201,703  
FILING DATE: 25-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,309  
FILING DATE: 13-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/621,502  
FILING DATE: 03-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8927546.5  
FILING DATE: 06-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5922846ak, Henry P.  
REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 4-17861/+/-Cont3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-789-588-26

Query Match 100.0%; Score 89; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2,1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14  
| | | | | | | | | | | | | | | | | | | | | |  
Db 6 FCLGPCPYIWSLDT 19

RESULT 3  
US-09-095-637D-4  
Sequence 4, Application US/09095637D  
Patent No. 6500920  
GENERAL INFORMATION:  
APPLICANT: HUANG, Jung S.  
TITLE OF INVENTION: AN INHIBITOR OF TRANSFORMING GROWTH FACTOR BETA AND A  
TITLE OF INVENTION: METHOD OF INHIBITING THE BIOLOGICAL EFFECTS OF  
TITLE OF INVENTION: TRANSFORMING GROWTH FACTOR BETA  
FILE REFERENCE: 16153-1637  
CURRENT APPLICATION NUMBER: US/09/095,637D  
CURRENT FILING DATE: 1998-06-11  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO: 4  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-095-637D-4

Query Match 100.0%; Score 89; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2,2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 FCLGPCPYIWSLDT 16

RESULT 4  
5168051-4  
Patent No. 5168051  
APPLICANT: DERYNCK, RIK M.A.;GOEDEL, DAVID V.  
TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES  
NUMBER OF SEQUENCES: 21  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/389,929  
FILING DATE: 04-AUG-1989  
SEQ ID NO:4;  
LENGTH: 51  
5168051-4

Query Match 100.0%; Score 89; DB 6; Length 51;  
Best Local Similarity 100.0%; Pred. No. 4,1e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14  
| | | | | | | | | | | | | | | | | | | | | |  
Db 34 FCLGPCPYIWSLDT 47

RESULT 5  
5168051-4  
Patent No. 5168051  
APPLICANT: DERYNCK, RIK M.A.;GOEDEL, DAVID V.  
TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES  
NUMBER OF SEQUENCES: 21  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/389,929  
FILING DATE: 04-AUG-1989  
SEQ ID NO:4;  
LENGTH: 51

5168051-4

Query Match 100.0%; Score 89; DB 6; Length 51;

Best Local Similarity 100.0%; Pred. No. 4.1e-05; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGCPYIWSLDT 14  
|||  
Db 34 FCLGCPYIWSLDT 47

RESULT 6  
US-09-363-939A-122

; Sequence 122, Application US/09363939A

; Patent No. 6346611

; GENERAL INFORMATION:

; APPLICANT: Pagratlis, Nikos

; APPLICANT: Lochrie, Michael

; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and

; TITLE OF INVENTION: Inhibitors

; FILE REFERENCE: NEX87

; CURRENT APPLICATION NUMBER: US/09/363,939A

; CURRENT FILING DATE: 1999-07-29

; PRIOR APPLICATION NUMBER: 09/046,247

; PRIOR FILING DATE: 1998-03-23

; PRIOR APPLICATION NUMBER: 08/458,424

; PRIOR FILING DATE: 1995-06-02

; PRIOR APPLICATION NUMBER: 07/714,131

; PRIOR FILING DATE: 1991-06-10

; PRIOR APPLICATION NUMBER: 07/931,473

; PRIOR FILING DATE: 1992-08-17

; PRIOR APPLICATION NUMBER: 07/964,624

; PRIOR FILING DATE: 1992-10-21

; PRIOR APPLICATION NUMBER: 08/117,991

; PRIOR FILING DATE: 1993-09-08

; PRIOR APPLICATION NUMBER: 07/536,428

; PRIOR FILING DATE: 1990-06-11

; NUMBER OF SEQ ID NOS: 216

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 122

; LENGTH: 60

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; US-09-363-939A-122

QY 1 FCLGCPYIWSLDT 14  
|||  
Db 43 FCLGCPYIWSLDT 56

RESULT 7  
US-09-791-301-122

; Sequence 122, Application US/09791301

; Patent No. 6713616

; GENERAL INFORMATION:

; APPLICANT: Pagratlis, Nikos

; APPLICANT: Lochrie, Michael

; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and

; TITLE OF INVENTION: Inhibitors

; FILE REFERENCE: NEX 87/C

; CURRENT APPLICATION NUMBER: US/09/791,301

; CURRENT FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: 09/046,247

; PRIOR FILING DATE: 1998-03-23

; PRIOR APPLICATION NUMBER: 08/458,424

; PRIOR FILING DATE: 1995-06-02

; PRIOR APPLICATION NUMBER: 07/714,131

; PRIOR FILING DATE: 1991-06-10

; PRIOR APPLICATION NUMBER: 07/931,473

; PRIOR FILING DATE: 1992-08-17

; PRIOR APPLICATION NUMBER: 07/964,624

; PRIOR FILING DATE: 1992-10-21

; PRIOR APPLICATION NUMBER: 08/117,991

; PRIOR FILING DATE: 1993-09-08

; PRIOR APPLICATION NUMBER: 07/536,428

; PRIOR FILING DATE: 1990-06-11

; PRIOR APPLICATION NUMBER: 09/363,939

; PRIOR FILING DATE: 1999-07-29

; NUMBER OF SEQ ID NOS: 216

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 122

; LENGTH: 60

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; US-09-791-301-122

QY 1 FCLGCPYIWSLDT 14  
|||  
Db 43 FCLGCPYIWSLDT 56

RESULT 8  
US-09-848-664A-9

; Sequence 9, Application US/09848664A

; Patent No. 6723344

; GENERAL INFORMATION:

; APPLICANT: Sakiyama-Bibert, Shelly E.

; TITLE OF INVENTION: Controlled Release of No. 6723344-Heparin Binding Growth

; TITLE OF INVENTION: Factors from Heparin Containing Matrices

; FILE REFERENCE: ETH 108

; CURRENT APPLICATION NUMBER: US/09/848,664A

; CURRENT FILING DATE: 2001-05-03

; PRIOR APPLICATION NUMBER: US/09/298,084A

; PRIOR FILING DATE: 1999-04-22

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 70

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-848-664A-9

QY 1 FCLGCPYIWSLDT 14  
|||  
Db 43 FCLGCPYIWSLDT 56

RESULT 9  
US-08-478-097A-1

; Sequence 1, Application US/08478097A

; Patent No. 6040431

; GENERAL INFORMATION:

; APPLICANT: KECK, PETER

; APPLICANT: SMART, JOHN

; TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B

TITLE OF INVENTION: SUPERFAMILY (MORPHONS)  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
STREET: THIBEAULT, LLP  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,097A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER ESQ, EDMUND R  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-080  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..98  
OTHER INFORMATION: /note= "TGF-B1 SEQUENCE"  
US-08-478-097A-1  
Query Match 100.0%; Score 89; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 7,2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FCLGPCPYIWSLDT 14  
Db 29 FCLGPCPYIWSLDT 42  
RESULT 10  
US-08-931-858E-150  
Sequence 150, Application US/08931858E  
Patent No. 6222022  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, EUGENE M  
APPLICANT: MILBRANDT, JEFFREY D  
APPLICANT: KOTZBAUER, PAUL T  
APPLICANT: LAMPE, PATRICIA A  
APPLICANT: KLEIN, ROBERT  
APPLICANT: DESAUVAGE, FRED  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
NUMBER OF SEQUENCES: 239  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MO  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,858E  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971486  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 314-727-5188  
TELEFAX: 314-727-6092  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-931-858E-150  
Query Match 100.0%; Score 89; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 7,2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FCLGPCPYIWSLDT 14  
Db 29 FCLGPCPYIWSLDT 42  
RESULT 11  
US-08-981-739-150  
Sequence 150, Application US/08981739  
Patent No. 6232449  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
APPLICANT: MILBRANDT, JEFFREY D.  
APPLICANT: KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/981,739  
FILING DATE: 31-Aug-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/03461  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 150:  
US-08-981-739-150

Query Match 100.0%; Score 89; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 7.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14  
|||  
Db 29 FCLGPCPYIWSLDT 42

RESULT 12  
US-09-128-026-150  
; Sequence 150, Application US/09128026  
; Patent No. 6403335  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOMEL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/128,026  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 976163  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 150:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-128-026-150

Query Match 100.0%; Score 89; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 7.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14  
|||  
Db 29 FCLGPCPYIWSLDT 42

RESULT 13  
US-09-496-398-1  
; Sequence 1, Application US/09496398  
; Patent No. 6479643  
; GENERAL INFORMATION:  
; APPLICANT: KECK, PETER  
; APPLICANT: SMART, JOHN  
; TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B  
; TITLE OF INVENTION: SUPERFAMILY (MORPHONS)

NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &  
ADDRESSEE: THIBEAULT, LLP  
STREET: 125 HIGH STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/496,398  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,097  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER ESQ, EDMUND R  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: STK-059CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..98  
OTHER INFORMATION: /note="TGF-B1 SEQUENCE"  
US-09-496-398-1

Query Match 100.0%; Score 89; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 7.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14  
|||  
Db 29 FCLGPCPYIWSLDT 42

RESULT 14  
US-09-220-616-150  
; Sequence 150, Application US/09220616  
; Patent No. 6645937  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOMEL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/220,616  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/981,739  
FILING DATE: 31-Aug-1998  
APPLICATION NUMBER: PCT/US97/03461  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE//DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-220-616-150

Query Match 100.0%; Score 89; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 7.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14  
|||||  
Db 29 FCLGPCPYIWSLDT 42

RESULT 15  
US-09-374-958C-40  
Sequence 40, Application US/09374958C  
Patent No. 6677432  
GENERAL INFORMATION:  
APPLICANT: Stryker Corporation  
TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including  
FILE REFERENCE: STR-076  
CURRENT APPLICATION NUMBER: US/09/374,958C  
CURRENT FILING DATE: 1999-08-16  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: PatentIn version 2.0  
SEQ ID NO 40  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: TGF-Beta1  
US-09-374-958C-40

Query Match 100.0%; Score 89; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 7.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14  
|||||  
Db 29 FCLGPCPYIWSLDT 42

Search completed: June 14, 2005, 16:10:14  
Job time : 20.7308 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:46:34 ; Search time 22.2115 Seconds  
(without alignments)  
50.412 Million cell updates/sec

Title: US-09-831-253f-1  
Perfect score: 96  
Sequence: 1 HANFCLGPCFYWSL 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	23	1	US-08-486-057B-26
2	96	100.0	23	2	US-08-789-588-26
3	96	100.0	51	6	5168051-4
4	96	100.0	51	6	5168051-4
5	96	100.0	60	3	US-09-363-939A-122
6	96	100.0	60	4	US-09-791-301-122
7	96	100.0	70	4	US-09-848-664A-9
8	96	100.0	70	4	US-08-478-097A-1
9	96	100.0	98	3	US-08-931-858B-150
10	96	100.0	98	3	US-08-981-739-150
11	96	100.0	98	4	US-09-128-026-150
12	96	100.0	98	4	US-09-496-398-1
13	96	100.0	98	4	US-09-220-616-150
14	96	100.0	98	4	US-09-374-958C-40
15	96	100.0	98	4	US-09-220-527-150
16	96	100.0	98	4	US-09-220-407-150
17	96	100.0	112	1	US-07-979-441-1
18	96	100.0	112	1	US-08-197-792-36
19	96	100.0	112	1	US-08-486-057B-41
20	96	100.0	112	1	US-08-459-850-36
21	96	100.0	112	1	US-08-459-214-36
22	96	100.0	112	1	US-08-470-837-30
23	96	100.0	112	2	US-08-789-588-41
24	96	100.0	112	2	US-08-410-573-1
25	96	100.0	112	2	US-09-123-233-2
26	96	100.0	112	3	US-08-927-433-5
27	96	100.0	112	3	US-08-868-453-30

28	96	100.0	112	4	US-09-095-637D-1	Sequence 1, Appl
29	96	100.0	112	5	PCT-US93-03068-1	Sequence 1, Appl
30	96	100.0	114	1	US-08-481-377-23	Sequence 23, Appl
31	96	100.0	114	2	US-08-491-835-21	Sequence 21, Appl
32	96	100.0	114	3	US-09-153-733A-23	Sequence 23, Appl
33	96	100.0	114	3	US-08-946-092A-21	Sequence 21, Appl
34	96	100.0	114	3	US-09-172-062-21	Sequence 21, Appl
35	96	100.0	114	3	US-08-624-635-22	Sequence 21, Appl
36	96	100.0	114	3	US-09-301-530D-21	Sequence 21, Appl
37	96	100.0	114	3	US-09-389-705-23	Sequence 23, Appl
38	96	100.0	114	5	PCT-US94-00666-23	Sequence 23, Appl
39	96	100.0	114	5	PCT-US94-00685-21	Sequence 21, Appl
40	96	100.0	115	1	US-08-581-529B-19	Sequence 19, Appl
41	96	100.0	115	1	US-08-455-559-25	Sequence 25, Appl
42	96	100.0	115	2	US-08-525-559B-29	Sequence 29, Appl
43	96	100.0	115	2	US-08-581-528A-19	Sequence 19, Appl
44	96	100.0	115	3	US-09-097-616-19	Sequence 19, Appl
45	96	100.0	115	3	US-09-177-860A-29	Sequence 29, Appl

## ALIGNMENTS

RESULT 1  
US-08-486-057B-26  
; Sequence 26, Application US/08486057B  
; Patent No. 5650494  
; GENERAL INFORMATION:  
; APPLICANT: Cerletti, Nico  
; APPLICANT: McMaster, Gary K.  
; APPLICANT: Cox, David  
; APPLICANT: Schmitz, Albert  
; APPLICANT: Meyhack, Bernd  
; TITLE OF INVENTION: Process for Refolding Recombinantly  
; TITLE OF INVENTION: Produced TGF-beta-like Proteins  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Henry P. No. 5650494k  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,057B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/201,703  
; FILING DATE: 25-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/960,309  
; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/621,502  
; FILING DATE: 03-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8927546.5  
; FILING DATE: 06-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5650494k, Henry P.  
; REGISTRATION NUMBER: 33200  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-486-057B-26

Query Match 100.0%; Score 96; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1,4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYIWSL 15  
|||||  
Db 3 HANFCLGPCPYIWSL 17

## RESULT 2

US-08-789-588-26  
Sequence 26, Application US/08789588  
Patent No. 5922846

GENERAL INFORMATION:  
APPLICANT: Cellecti, Nicco  
APPLICANT: McMaster, Gary K.  
APPLICANT: Cox, David  
APPLICANT: Schmitz, Albert  
APPLICANT: Meyhack, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly  
TITLE OF INVENTION: Produced TGF-beta-like Proteins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Henry P. No. 5922846ak  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-9005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/789,588  
FILING DATE:

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/486,057  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/201,703  
FILING DATE: 25-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,309  
FILING DATE: 13-OCT-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/621,502  
FILING DATE: 03-DEC-1990  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8927546.5  
FILING DATE: 06-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5922846ak, Henry P.

REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 4-17861/-/Cont3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110

INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids

TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-789-588-26

Query Match 100.0%; Score 96; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1,4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYIWSL 15  
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Db 3 HANFCLGPCPYIWSL 17

## RESULT 3

5168051-4  
Patent No. 5168051  
APPLICANT: DERYNCK, RIK M.A.;GOEDEL, DAVID V.  
TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES  
NUMBER OF SEQUENCES: 21  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/389,929  
FILING DATE: 04-AUG-1989  
SEQ ID NO: 4:  
LENGTH: 51

5168051-4

Query Match 100.0%; Score 96; DB 6; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2,8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYIWSL 15  
|||||  
Db 31 HANFCLGPCPYIWSL 45

## RESULT 4

5168051-4  
Patent No. 5168051  
APPLICANT: DERYNCK, RIK M.A.;GOEDEL, DAVID V.  
TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES  
NUMBER OF SEQUENCES: 21  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/389,929  
FILING DATE: 04-AUG-1989  
SEQ ID NO: 4:  
LENGTH: 51

5168051-4

Query Match 100.0%; Score 96; DB 6; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2,8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYIWSL 15  
|||||  
Db 31 HANFCLGPCPYIWSL 45

## RESULT 5

US-09-363-939A-122  
Sequence 122, Application US/09363939A  
Patent No. 6346611  
GENERAL INFORMATION:  
APPLICANT: Pagratlis, Nikos  
APPLICANT: Lochrie, Michael  
APPLICANT: Gold, Larry  
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
TITLE OF INVENTION: Inhibitors

FILE REFERENCE: NEX87  
CURRENT APPLICATION NUMBER: US/09/363,939A  
CURRENT FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: 09/046,247  
PRIOR FILING DATE: 1998-03-23

PRIOR APPLICATION NUMBER: 08/458,424  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: 07/714,131



PRIOR FILING DATE: 1991-06-10  
PRIOR APPLICATION NUMBER: 07/931,473  
PRIOR FILING DATE: 1992-08-17  
PRIOR APPLICATION NUMBER: 07/964,624  
PRIOR FILING DATE: 1992-10-21  
PRIOR APPLICATION NUMBER: 08/117,991  
PRIOR FILING DATE: 1993-09-08  
PRIOR APPLICATION NUMBER: 07/536,428  
PRIOR FILING DATE: 1990-06-11  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 122  
LENGTH: 60  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-363-939A-122

Query Match 100.0%; Score 96; DB 3; Length 60;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGCPYIWSL 15  
Db 40 HANFCLGCPYIWSL 54

RESULT 6  
US-09-791-301-122  
Sequence 122, Application US/09791301  
Patent No. 6713616  
GENERAL INFORMATION:  
APPLICANT: Pagratlis, Nikos  
APPLICANT: Lochrie, Michael  
APPLICANT: Gold, Larry  
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
TITLE OF INVENTION: Inhibitors  
FILE REFERENCE: NEX 87/C  
CURRENT APPLICATION NUMBER: US/09/791,301  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/046,247  
PRIOR FILING DATE: 1998-03-23  
PRIOR APPLICATION NUMBER: 08/458,424  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: 07/714,131  
PRIOR FILING DATE: 1991-06-10  
PRIOR APPLICATION NUMBER: 07/931,473  
PRIOR FILING DATE: 1992-08-17  
PRIOR APPLICATION NUMBER: 07/964,624  
PRIOR FILING DATE: 1992-10-21  
PRIOR APPLICATION NUMBER: 08/117,991  
PRIOR FILING DATE: 1993-09-08  
PRIOR APPLICATION NUMBER: 07/536,428  
PRIOR FILING DATE: 1990-06-11  
PRIOR APPLICATION NUMBER: 09/363,939  
PRIOR FILING DATE: 1999-07-29  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 122  
LENGTH: 60  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-791-301-122

Query Match 100.0%; Score 96; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGCPYIWSL 15  
Db 40 HANFCLGCPYIWSL 54

RESULT 7  
US-09-848-664A-9  
Sequence 9, Application US/09848664A  
Patent No. 6723344  
GENERAL INFORMATION:  
APPLICANT: Sakiyama-Elbert, Shelly E.  
APPLICANT: Hubbell, Jeffrey A.  
TITLE OF INVENTION: Controlled Release of No. 6723344-Heparin Binding Growth  
FILE REFERENCE: ETH 108  
CURRENT APPLICATION NUMBER: US/09/848,664A  
CURRENT FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: US/09/298,084A  
PRIOR FILING DATE: 1999-04-22  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 9  
LENGTH: 70  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-848-664A-9

Query Match 100.0%; Score 96; DB 4; Length 70;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGCPYIWSL 15  
Db 40 HANFCLGCPYIWSL 54

RESULT 8  
US-08-478-097A-1  
Sequence 1, Application US/08478097A  
Patent No. 6040431  
GENERAL INFORMATION:  
APPLICANT: KECK, PETER  
APPLICANT: SMART, JOHN  
TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B  
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &  
ADDRESSEE: THIBEAULT, LLP  
STREET: 125 HIGH STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,097A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER ESQ, EDMUND R  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-080  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: protein  
LOCATION: 1..98  
OTHER INFORMATION: /note="TGF-B1 SEQUENCE"  
US-08-478-097A-1

Query Match 100.0%; Score 96; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFLGCPYIWSL 15  
|||  
DB 26 HANFLGCPYIWSL 40

RESULT 9  
US-08-931-858E-150  
Sequence 150, Application US/08931858E  
Patent No. 6222022  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, EUGENE M  
APPLICANT: MILBRANDT, JEFFREY D  
APPLICANT: KOTZBAUER, PAUL T  
APPLICANT: LAMPE, PATRICIA A  
APPLICANT: KLEIN, ROBERT  
APPLICANT: DESAUVAGE, FRED  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
NUMBER OF SEQUENCES: 239  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MO  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,858E  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971486  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 314-727-5188  
TELEFAX: 314-727-6092  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-931-858E-150

Query Match 100.0%; Score 96; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFLGCPYIWSL 15  
|||  
DB 26 HANFLGCPYIWSL 40

RESULT 10  
US-08-981-739-150  
Sequence 150, Application US/08981739  
Patent No. 6232449

GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
MILBRANDT, JEFFREY D.  
KOTZBAUER, PAUL T.  
LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/981,739  
FILING DATE: 31-Aug-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/03461  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 150:  
US-08-981-739-150

Query Match 100.0%; Score 96; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFLGCPYIWSL 15  
|||  
DB 26 HANFLGCPYIWSL 40

RESULT 11  
US-09-128-026-150  
Sequence 150, Application US/09128026  
Patent No. 640335

GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
APPLICANT: MILBRANDT, JEFFREY D.  
APPLICANT: KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US

```

; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,026
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-128-026-150

Query Match      100.0%; Score 96; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HANFCLGPCPYIWSL 15
        |||||
Db      26 HANFCLGPCPYIWSL 40

RESULT 12
US-09-496-398-1
; Sequence 1, Application US/09496398
; Patent No. 6479643
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: SMART, JOHN
; TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B
; TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT, LLP
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/496,398
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,097
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STX-059CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7000
; TELEFAX: 617-248-7100
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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..98
; OTHER INFORMATION: /note="TGF-B1 SEQUENCE"
; US-09-496-398-1

Query Match      100.0%; Score 96; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HANFCLGPCPYIWSL 15
        |||||
Db      26 HANFCLGPCPYIWSL 40

RESULT 13
US-09-220-616-150
; Sequence 150, Application US/09220616
; Patent No. 6645937
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,616
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,739
; FILING DATE: 31-AUG-1998
; APPLICATION NUMBER: PCT/US97/03461
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-220-616-150

Query Match      100.0%; Score 96; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HANFCLGCPYIWSL 15  
|||  
Db 26 HANFCLGCPYIWSL 40

RESULT 14  
US-09-374-958C-40  
Sequence 40, Application US/09374958C  
Patent No. 6677432  
GENERAL INFORMATION:  
APPLICANT: STRYKER Corporation  
TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including  
FILE REFERENCE: STK-076  
CURRENT APPLICATION NUMBER: US/09/374,958C  
CURRENT FILING DATE: 1999-08-16  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: PatentIn version 2.0  
SEQ ID NO 40  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: TGF-Beta1  
US-09-374-958C-40

Query Match 100.0%; Score 96; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. NO. 5.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15  
|||  
Db 26 HANFCLGCPYIWSL 40

RESULT 15  
US-09-220-527-150  
Sequence 150, Application US/09220527  
Patent No. 6692943  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
MILBRANDT, JEFFREY D.  
KOTZBAUER, PAUL T.  
LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/220,527  
FILING DATE: 24-Dec-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/981,739  
FILING DATE: 31-Aug-1998  
APPLICATION NUMBER: PCT/US97/03461  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 150:  
US-09-220-527-150

Query Match 100.0%; Score 96; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. NO. 5.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15  
|||  
Db 26 HANFCLGCPYIWSL 40

Search completed: June 14, 2005, 16:10:14  
Job time : 23.215 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: June 14, 2005, 15:29:15 ; Search time 85.9615 Seconds  
(without alignments)  
67.488 Million cell updates/sec

Title: US-09-831-253f-1  
Perfect score: 96  
Sequence: 1 HANFLGRCFYIWSL 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

1: Genesepq\_16Dec04:\*  
2: Genesepq\_1980s:\*  
3: Genesepq\_1990s:\*  
4: Genesepq\_2000s:\*  
5: Genesepq\_2001s:\*  
6: Genesepq\_2003as:\*  
7: Genesepq\_2003bs:\*  
8: Genesepq\_2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	15	3	AAV92965 Transform
2	96	100.0	15	3	AAV92945 Transform
3	96	100.0	23	3	AAV92983 Transform
4	96	100.0	23	3	AAV92954 Transform
5	96	100.0	50	2	AAV90828 Pre-trans
6	96	100.0	51	2	AAV904075 Sequence
7	96	100.0	51	4	AAV78788 Human tra
8	96	100.0	51	4	AAV43879 Peptide #
9	96	100.0	51	4	AAV37799 Peptide #
10	96	100.0	51	4	AAV77605 Human Don
11	96	100.0	51	5	ABG46640 Human pep
12	96	100.0	62	2	AAV68685 Human TGF
13	96	100.0	62	2	AAV30331 Fragment
14	96	100.0	65	2	AAV22135 PDGI subu
15	96	100.0	98	2	AAV16697 MO9914235
16	96	100.0	98	3	AAV92554 TGF-beta
17	96	100.0	98	3	AAV09519 Human TGF
18	96	100.0	98	3	AAV02785 Human TGF
19	96	100.0	112	2	AAV08142 Placental
20	96	100.0	112	2	AAV04076 Sequence
21	96	100.0	112	2	AAV12402 Transform
22	96	100.0	112	2	AAV22134 PDGI subu
23	96	100.0	112	2	AAV43263 TGF-beta
24	96	100.0	112	2	AAV42311 Recombina
25	96	100.0	112	2	AAV92773 Human TGF

26	96	100.0	112	2	AAV91956 Human tra
27	96	100.0	112	2	AAV08173 TGF-beta
28	96	100.0	112	2	AAV78781 Human tra
29	96	100.0	112	2	AAV97091 The matur
30	96	100.0	112	2	AAV08299 Human gro
31	96	100.0	112	2	AAV84207 Transform
32	96	100.0	112	3	AAV67950 Human tra
33	96	100.0	112	3	AAV92010 Human tra
34	96	100.0	112	4	AAV35937 TGF-beta
35	96	100.0	112	5	AAV51939 Human TGF
36	96	100.0	112	6	AAV08656 Human tra
37	96	100.0	112	8	AAV11598 Human bon
38	96	100.0	112	8	AAV79530 Human tra
39	96	100.0	114	2	AAV39638 Human tra
40	96	100.0	115	4	AAV73204 TGF-beta
41	96	100.0	115	6	AAV76033 Human TGF
42	96	100.0	118	2	AAV08176 TGF-beta
43	96	100.0	120	8	AAV17006 Porcine T
44	96	100.0	120	8	AAV17010 Porcine T
45	96	100.0	122	2	AAV08181 TGF-beta

## ALIGNMENTS

RESULT 1  
ID AAV92965 standard; peptide, 15 AA.  
AAV92965;  
08-NOV-2000 (first entry)  
Transforming growth factor inhibitory peptide P11.  
Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;  
Competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
extracellular matrix degradation inhibitor; mimotope; cirrhosis.  
Homo sapiens.  
WO2000031135-A1.  
02-JUN-2000.  
23-NOV-1999; 99WO-ES000375.  
24-NOV-1998; 98ES-00002465.  
(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
Ezquerro Saenz JI, Lasarte Sagastibelza JI, Prieto Valtuena J;  
Borras Cuesta F;  
WPI, 2000-411935/35.  
Peptides that antagonize binding of transforming growth factor beta1,  
useful for treatment of liver disease, especially cirrhosis, are partial  
sequences of the factor or its receptors.  
Disclosure; Page 22; 86pp; Spanish.  
The invention relates to synthetic peptides that antagonize the binding  
of transforming growth (TGF) Factor beta1 (TGF-beta1) to its receptor in  
vivo which have partial amino acid sequences identical, or similar, with  
those of TGF-beta1 and/or its receptors. Peptides AAV92945-Y93133 represent  
examples of the peptides of the invention. The peptides act by  
competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.  
they are inhibitors of stimulation of collagen synthesis in liver cells  
and inhibitors of synthesis of proteolytic enzymes able to degrade the  
extracellular matrix. The peptides, their mimetopes and/or DNA (or  
expression systems) encoding the peptides are used for treatment of liver  
disease, specifically cirrhosis

XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 96; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYIWSL 15  
DB 1 HANFCLGPCPYIWSL 15

## RESULT 2

AA92945  
ID AA92945 standard; peptide; 15 AA.

AC AA92945;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide #1.

KM Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;  
KM competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KM extracellular matrix degradation inhibitor; mimotope; cirrhosis.

OS Homo sapiens.

PN WO200031135-A1.

PD 02-JUN-2000.

PF 23-NOV-1999; 99WO-ES000375.

PR 24-NOV-1998; 98ES-00002465.

PA (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.

PI Ezquerro Saenz JI, Lasarte Sagastibelza JI, Prieto Valtuena J;

PI Borras Cuesta F;

DR WPI; 2000-411935/35.

PT Peptides that antagonize binding of transforming growth factor betaf,  
PT useful for treatment of liver disease, especially cirrhosis, are partial  
PT sequences of the factor or its receptors.

PS Claim 2; Page 80; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in  
CC vivo which have partial amino acid sequences identical, or similar, with  
CC those of TGF-b1 and/or its receptors. Peptides AA92945-Y93133 represent  
CC examples of the peptides of the invention. The peptides act by  
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
CC they are inhibitors of stimulation of collagen synthesis in liver cells  
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
CC expression systems) encoding the peptides are used for treatment of liver  
CC disease, specifically cirrhosis

XX Sequence 15 AA;

Query Match 100.0%; Score 96; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYIWSL 15  
DB 1 HANFCLGPCPYIWSL 15

## RESULT 3

AA92983  
ID AA92983 standard; peptide; 23 AA.

AC AA92983;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide P29.

KM Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;  
KM competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KM extracellular matrix degradation inhibitor; mimotope; cirrhosis.

OS Homo sapiens.

PN WO200031135-A1.

PD 02-JUN-2000.

PF 23-NOV-1999; 99WO-ES000375.

PR 24-NOV-1998; 98ES-00002465.

PA (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.

PI Ezquerro Saenz JI, Lasarte Sagastibelza JI, Prieto Valtuena J;

PI Borras Cuesta F;

DR WPI; 2000-411935/35.

PT Peptides that antagonize binding of transforming growth factor betaf,  
PT useful for treatment of liver disease, especially cirrhosis, are partial  
PT sequences of the factor or its receptors.

PS Disclosure; Page 24; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in  
CC vivo which have partial amino acid sequences identical, or similar, with  
CC those of TGF-b1 and/or its receptors. Peptides AA92945-Y93133 represent  
CC examples of the peptides of the invention. The peptides act by  
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
CC they are inhibitors of stimulation of collagen synthesis in liver cells  
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
CC expression systems) encoding the peptides are used for treatment of liver  
CC disease, specifically cirrhosis

XX Sequence 23 AA;

Query Match 100.0%; Score 96; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYIWSL 15  
DB 7 HANFCLGPCPYIWSL 21

## RESULT 4

AA92954  
ID AA92954 standard; peptide; 23 AA.

AC AA92954;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide #10.

KM Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;  
KM competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KM extracellular matrix degradation inhibitor; mimotope; cirrhosis.

OS Homo sapiens.  
 XX  
 XX WO200031135-A1.  
 XX  
 PD 02-JUN-2000.  
 XX  
 XX 23-NOV-1999; 99WO-ES000375.  
 XX  
 XX 24-NOV-1998; 98ES-00002465.  
 XX  
 PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
 XX  
 PI Ezquerro Saenz JI, Lasaarte Sagastibelza JJ, Prieto Valcuna J;  
 PI Borras Cuesta F;  
 XX  
 DR WPI, 2000-411935/35.  
 XX  
 PT Peptides that antagonize binding of transforming growth factor beta1,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.  
 XX  
 PS Claim 11; Page 82; 86pp; Spanish.  
 XX  
 CC The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor beta1 (TGF-β1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-β1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-β1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 23 AA;  
 XX  
 Query Match 100.0%; Score 96; DB 3; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HANFCLGCPYIMSL 15  
 DB 7 HANFCLGCPYIMSL 21  
 XX  
 RESULT 5  
 AAR90828  
 ID AAR90828 standard; peptide; 50 AA.  
 XX  
 AC AAR90828;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 25-JAN-1980 (first entry)  
 XX  
 DE Pre-transforming growth factor beta 1 residues 252 to 302.  
 XX  
 KW transforming growth factor beta 1; wound healing; recombinant production.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US5482851-A.  
 PN  
 XX 09-JAN-1996.  
 PD  
 XX  
 PF 05-NOV-1993; 93US-00147364.  
 XX  
 PR 22-MAR-1985; 85US-00715142.  
 PR 13-MAR-1987; 87US-00025423.  
 PR 04-AUG-1989; 89US-0038929.  
 PR 04-MAR-1992; 92US-00845893.  
 XX  
 PA (GETH ) GENENTECH INC.

XX  
 PI Goeddel DV, Derynck RMA;  
 XX  
 DR WPI, 1996-076891/08.  
 DR N-PSDB; AAT15721.  
 XX  
 PT New recombinant human transforming growth factor-beta prods. - produced  
 PT using Chinese hamster ovary cells, for use in diagnostic applications or  
 PT in therapy.  
 XX  
 PS Example 2; Fig 2; 26pp; English.  
 XX  
 CC The transforming growth factor (TGF) beta 1 exon (residues 252 to 302)  
 CC was identified using the "long probe" strategy used previously for TGF-  
 CC alpha. Long oligonucleotides (T1572-23) designed on the basis of the  
 CC partial protein sequence were used as hybridisation probes for the exon  
 CC in a human genomic DNA library. The TGF beta 1 exon was then used as a  
 CC probe for the isolation of TGF beta 1 cDNA (see AAT15270). DNA encoding  
 CC TGF beta 1 is useful for the recombinant production of the protein, which  
 CC is useful in, e.g. wound healing. (Updated on 25-MAR-2003 to correct PF  
 CC field.)  
 XX  
 SQ Sequence 50 AA;  
 XX  
 Query Match 100.0%; Score 96; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HANFCLGCPYIMSL 15  
 DB 31 HANFCLGCPYIMSL 45  
 XX  
 RESULT 6  
 AAR04075  
 ID AAR04075 standard; protein; 51 AA.  
 XX  
 AC AAR04075;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 31-OCT-2002 (revised)  
 DT 31-MAY-1989 (first entry)  
 XX  
 DE Sequence of genomic fragment encoding a TGF-beta 1 exon.  
 XX  
 KW Transforming growth factor beta-3 (TGF beta 3); tumour cells;  
 KW growth inhibition.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W08912101-A.  
 PN  
 PD 14-DEC-1989.  
 PD  
 PF 08-JUN-1988; 88WO-US001945.  
 PF  
 PR 08-JUN-1988; 88WO-US001945.  
 PR  
 XX (GETH ) GENENTECH INC.  
 PA  
 PI Derynck RMA, Goeddel DV;  
 XX  
 DR WPI, 1990-007474/01.  
 DR P-PSDB; AAR04075.  
 DR  
 PT Nucleotide sequence encoding transforming growth factor beta-3 - used as  
 PT a probe, or to produce tgf beta-3, for growth inhibition of certain  
 PT normal and neoplastic cells, e.g. A549.  
 XX  
 PS Disclosure; Fig 2; 61pp; English.  
 XX  
 CC This sequence encodes an exon of transforming growth factor-beta 1 (TGF-  
 CC beta 1) polypeptide corresponding to AA's 288-338 of mature TGF-beta 1.

CC The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and CC neoplastic cell growth inhibition. (Updated on 31-OCT-2002 to add missing CC OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)

CC Sequence 51 AA;

Query Match 100.0%; Score 96; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15  
Db 31 HANFCLGCPYIWSL 45

RESULT 7  
AAW78788  
ID AAW78788 standard; protein; 51 AA.

XX AAW78788;  
XX 25-MAR-2003 (revised)  
DT 21-DEC-1998 (first entry)

XX Human transforming growth factor-beta fragment (aa288-338).

XX Transforming growth factor-beta 1; TGF-beta 1; human.

XX Homo sapiens.

XX US5801231-A.

XX 01-SEP-1998.

XX 30-MAY-1995; 95US-00454468.

XX 22-MAR-1985; 85US-00715142.

XX 13-MAR-1987; 87US-00025423.

XX 04-AUG-1989; 89US-00389929.

XX 04-MAR-1992; 92US-00845893.

XX 05-NOV-1993; 93US-00147364.

XX (GERTH ) GENENTECH INC.

XX Derynck RNA, Goeddel DV;

XX WPI; 1998-494840/42.

XX N-PSDB; AAV52936.

XX DNA encoding transforming growth factor-beta precursor sequence - useful for analysis to perform manipulations to increase yield of recombinant production of the protein.

XX Example 2; Fig 2; 26pp; English.

XX This polypeptide comprises amino acid residues 288-338 of human transforming growth factor-beta 1 precursor (preTGF-beta 1, see also CC AAW78785). It is encoded by an isolated fragment (see AAV52936) of the TGF-beta 1 gene. The invention relates to the recombinant production of CC TGF-beta. Nucleic acids encoding TGF-beta have been isolated and cloned into vectors which are replicated in bacteria and expressed in eukaryotic CC cells. TGF-beta recovered from transformed cells is used in known CC therapeutic applications. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 51 AA;

Query Match 100.0%; Score 96; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15

Db 31 HANFCLGCPYIWSL 45

RESULT 8  
ABB43879  
ID ABB43879 standard; peptide; 51 AA.

XX ABB43879;

XX 04-FEB-2002 (first entry)

XX Peptide #11385 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.

XX Claim 27; SEQ ID NO 36514; 639pp + Sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The CC present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form CC part of the printed specification, but was obtained in electronic format CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 51 AA;

Query Match 100.0%; Score 96; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15  
Db 31 HANFCLGCPYIWSL 45

RESULT 9  
AAM37799

ID AAM37799 standard; protein; 51 AA.

XX AAM37799;

XX 17-OCT-2001 (first entry)

XX Peptide #11836 encoded by probe for measuring placental gene expression.



KW Probe; microarray; human; placenta; antenatal diagnosis;  
KM genetic disorder.  
XX  
OS Homo sapiens.  
XX WO200157272-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000663.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488897/53.  
XX  
DR Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.  
XX  
PS Claim 27; SEQ ID NO 38068; 654bp; English.  
XX  
XX The present invention relates to single exon nucleic acid probes (SENP;  
CC see AAI31315-AA157546). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for producing a microarray for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders  
CC  
SQ Sequence 51 AA;  
  
Query Match 100.0%; Score 96; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 HANFCLGCPYIWSL 15  
|||  
DB 31 HANFCLGCPYIWSL 45  
  
RESULT 10  
AAAM77605  
ID AAM77605 standard; protein; 51 AA.  
XX  
AC AAM77605;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human bone marrow expressed protein SEQ ID NO: 37911.  
XX  
KW Human; bone marrow expressed exon; gene expression analysis; probe;  
KW microarray; cancer; leukaemia; lymphoma; myeloma.  
XX  
OS Homo sapiens.  
XX  
PN WO200157276-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000668.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488900/53.  
XX  
DR Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human bone marrow.  
XX  
PS Example 4; SEQ ID NO 37911; 658bp + Sequence Listing; English.  
XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
CC protein encoded by one of the probes of the invention  
CC  
SQ Sequence 51 AA;  
  
Query Match 100.0%; Score 96; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 HANFCLGCPYIWSL 15  
|||  
DB 31 HANFCLGCPYIWSL 45  
  
RESULT 11  
ABG46640  
ID ABG46640 standard; peptide; 51 AA.  
XX  
AC ABG46640;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 36305.  
XX  
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
KW chronic obstructive pulmonary disease; interstitial lung disease;  
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsagen syndrome;  
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;  
KW hyaline membrane disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200186003-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000665.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI: 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to

PT measure gene expression in human lung samples.

XX

PS Claim 27; SEQ ID NO 36305; 634bp; English.

XX

CC The invention relates to a spatially-addressable set of single exon

CC nucleic acid probes for measuring gene expression in a sample derived of

CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their

CC complements or the 12617 open reading frames derived from the 12614

CC probes. Also included are a microarray comprising the novel set of probes

CC; the novel set of probes which hybridise at high stringency to a nucleic

CC acid expressed in the human lung; measuring gene expression in a sample

CC derived from human lung; comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human lung

CC mRNA, and (b) measuring the label detectably bound to each probe of the

CC array; identifying exons in a eukaryotic genome, comprising (a)

CC algorithmically predicting at least one exon from genomic sequences of

CC the eukaryote; and (b) detecting specific hybridisation of detectably

CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

CC having a fragment identical to the predicted exon, the probe is included

CC in the above mentioned microarray; assigning exons to a single gene,

CC comprising (a) identifying exons from genomic sequence by the method

CC above and (b) measuring the expression of each of the exons in several

CC tissues and/or cell types using hybridisation to a single exon

CC microarrays having a probe with the exon, where a common pattern of

CC expression of the exons in the tissues and/or cell types indicates that

CC the exons should be assigned to a single gene; a peptide comprising one

CC of 12011 sequences, mentioned in the specification, or encoded by the

CC probes/open reading frames (ORF). The probes are used for gene expression

CC analysis, and for identifying exons in a gene, particularly using human

CC lung derived mRNA and for the study of lung diseases such as asthma, lung

CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung

CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,

CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-

CC Pulak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary

CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,

CC Karaganeser syndrome, fibrocystic pulmonary dysplasia, primary ciliary

CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The

CC present sequence is a peptide/protein encoded by a single exon probe of

CC the invention. Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format

CC directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

XX

XX Sequence 51 AA;

SO

Query Match	100.0%	Score 96;	DB 5;	Length 51;
Best Local Similarity	100.0%;	Pred. No. 5.8e-06;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1 HANFCLGRCPTWTL 15			
DB	31 HANFCLGRCPTWTL 45			

RESULT 12

AAB68685

ID AAB68685 standard; protein; 60 AA.

XX

XX AAB68685;

AC

XX

DT 03-MAY-2001 (first entry)

DT

DE Human TGFbeta1 protein #1.

XX

XX Human; transforming growth factor beta2; TGFbeta2; SILEX;

KW systemic evolution of ligands by exponential enrichment.

XX

XX Homo sapiens.

XX

XX WO200109156-A1.

XX

```

XX 08-FEB-2001.
PD
XX
XX 26-JUL-2000; 2000WO-US020397.
PF
XX 29-JUL-1999; 99US-00363939.
PR
XX (NEXSTAR) NEXSTAR PHARM INC.
PA
XX Pagratis N, Lochrie M, Gold L;
PI
XX WPI; 2001-218217/22.
DR
XX
XX New RNA ligand to human transforming growth factor beta2, useful as
PT pharmaceuticals, diagnostics and as immunohistochemical reagents.
XX
XX Disclosure; Page 71, 178pp; English.
XX
XX The present invention relates to non-naturally occurring, high-affinity
CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
CC oligonucleotide ligands were identified by the SELEX method (SELEX stands
CC for Systematic Evolution of Ligands by EXponential ENrichment). The
CC oligonucleotide ligands are useful in any process in which binding to
CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,
CC diagnostics, imaging agents and immunohistochemical reagents
XX
XX Sequence 60 AA;
SQ
XX
XX Query Match 100.0%; Score 96; DB 4; Length 60;
XX Best Local Similarity 100.0%; Pred. No. 6,7e-06;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 1 HANFLGCPPIYWSL 15
QY |||||
XX 40 HANFLGCPPIYWSL 54
DB
XX
XX RESULT 13
XX AAM30331
XX ID AAM30331 standard; peptide; 62 AA.
XX
XX AAM30331;
XX
XX 11-FEB-1998 (first entry)
DT
XX
XX Fragment of growth factor TGFbeta1.
DE
XX
XX Neurturin; human; hematopoietic cell; neuronal cell; stem cell; NT gene;
KW neurodegenerative disease; peripheral neuropathy; nervous system tumour;
KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; ischemic stroke; acute brain injury; basopenia;
KW acute spinal cord injury; multiple sclerosis; eosinopenia; lymphopenia;
KW monocytopenia; neutropenia; anaemia; thrombocytopenia; neuroblastoma;
KW antibody; obesity; therapy; transforming growth factor beta; TGFbeta1;
KW growth factor; hybrid protein.
XX
XX Homo sapiens.
XX OS
XX WO9708196-A1.
XX PN
XX 06-MAR-1997.
XX PD
XX 27-AUG-1996; 96WO-US014065.
XX PF
XX 28-AUG-1995; 95US-00519777.
XX PR
XX (UNIW ) UNIV WASHINGTON.
XX PA
XX Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA;
XX WPI; 1997-179176/16.
XX DR
XX A novel growth factor Neurturin - used to treat neuro-degenerative and
PT

```

PT haematopoietic cell degeneration diseases, e.g. Alzheimer's disease and  
 PT eosinopenia.  
 PS  
 PS Claim 93; Fig 17; 206pp; English.  
 XX  
 CC AAW30331-W30353 represent human growth factor fragments that are used in  
 CC a hybrid polypeptide of the invention. These sequences form a hybrid with  
 CC the human neuturin (NT) fragment shown in AAW30378. NT promotes the  
 CC growth and differentiation of haematopoietic and neuronal cells, and  
 CC their stem cells. The NT gene and protein are used to prevent or treat  
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic  
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's  
 CC disease, ischaemic stroke, acute brain injury, acute spinal cord injury,  
 CC nervous system tumours, multiple sclerosis and infection; and  
 CC haematopoietic cell degenerative diseases, e.g. eosinopenia, basopenia,  
 CC lymphopenia, monocytopenia, neutropenia, anaemia, thrombocytopenia,  
 CC and stem cell insufficiencies. The NT protein and gene are also useful to  
 CC treat neuroblastomas. Antibodies against NT and oligonucleotides (used as  
 CC either probes or primers, corresponding to an exon of pre-pro-NT gene or  
 CC flanking a target sequence) can be used for detecting NT in a sample or  
 CC detecting mutations in the NT gene. Antisense sequences of the NT gene  
 CC are used to treat diseases promoted by NT expression e.g. obesity  
 CC  
 XX  
 SQ Sequence 62 AA;  
 Query Match 100.0%; Score 96; DB 2; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HANFCLGCPYIWSL 15  
 |||||  
 Db 26 HANFCLGCPYIWSL 40  
 |||||  
 RESULT 14  
 AAR2135  
 ID AAR2135 standard; peptide; 65 AA.  
 XX  
 AC AAR2135;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 10-JUL-1992 (first entry)  
 XX  
 XX PDGI subunit b.  
 DE  
 XX  
 XX Platelet derived growth inhibitor alpha; TGF-beta; trypsin; pepsin;  
 KW cell proliferation; eczema; immunosuppressant.  
 XX  
 XX Homo sapiens.  
 OS  
 XX EP475719-A.  
 PN  
 XX 18-MAR-1992.  
 PD  
 XX 10-SEP-1991; 91EP-00308239.  
 PF  
 XX 11-SEP-1990; 90JP-00238944.  
 PR  
 XX (NAKA/) NAKAMURA T.  
 PA  
 XX Nakamura T, Nakamura T;  
 PI  
 XX WPI; 1992-090304/12.  
 DR  
 XX  
 XX New platelet-derived growth regulating peptide-alpha - used for treatment  
 PT of eczema, stimulation of bone growth and as immunosuppressant.  
 PT  
 XX  
 PS Claim 2; Page 11; 21pp; English.  
 XX  
 CC The peptide is subunit b of PDGI alpha. It can be obtd. by treating  
 CC transforming growth factor (TGF) beta with chymotrypsin or pepsin, or can  
 CC be isolated from human blood platelets or by recombinant expression of  
 CC DNA obtd. using RNA extd. from blood plasma. PDGI alpha is comprised of

CC subunits a, b and c bonded b-a-c. PDGI alpha can be used for controlling  
 CC cell proliferation without the cancerous activity (transformation  
 CC activity) associated with TGF-beta. PGFI- alpha can be used for  
 CC activation and acceleration of the proliferation of epithelium cells in  
 CC treating eczema, for stimulating osseous growth for bone formation or as  
 CC an immuno- suppressant for immune diseases. See also AAR2134-6. (Updated  
 CC on 25-MAR-2003 to correct PF field.)  
 CC  
 XX  
 SQ Sequence 65 AA;  
 Query Match 100.0%; Score 96; DB 2; Length 65;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HANFCLGCPYIWSL 15  
 |||||  
 Db 40 HANFCLGCPYIWSL 54  
 |||||  
 RESULT 15  
 AAY1697  
 ID AAY1697 standard; peptide; 98 AA.  
 XX  
 XX AAY1697;  
 XX  
 DT 17-AUG-1999 (first entry)  
 DT  
 XX WO9914235 Seq ID No: 150.  
 DE  
 XX  
 KW Growth factor; GF; persephin; neuron growth; cellular degeneration;  
 KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma;  
 KW brain injury; spinal cord injury; nervous system tumor; infection;  
 KW multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin;  
 KW metabolic disease; diabetes; renal dysfunction; neuturin.  
 XX  
 XX Unidentified.  
 OS  
 XX WO9914235-A1.  
 PN  
 XX 25-MAR-1999.  
 PD  
 XX 15-SEP-1998; 98WO-US019163.  
 PF  
 XX 16-SEP-1997; 97US-00931858.  
 PR  
 XX (UNIW ) UNIV WASHINGTON.  
 PA  
 XX Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA, Klein R;  
 PI Desauvage F;  
 PI WPI; 1999-244023/20.  
 DR  
 XX  
 XX New isolated persephin growth factor nucleic acids used to, e.g. promote  
 PT neuronal growth.  
 PT  
 XX  
 PS Disclosure; Page 175-176; 222pp; English.  
 XX  
 CC The invention relates to a novel isolated and purified growth factor (GF)  
 CC that comprises persephin or a fragment or a conservatively substituted  
 CC variant. The persephin GF polypeptides can promote the survival and  
 CC growth of neurons and non-neuronal cells. The persephin GF polypeptides  
 CC or polynucleotides can be used for preventing or treating cellular  
 CC degeneration or insufficiency, e.g. neuronal degeneration resulting from  
 CC peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, ischemic stroke,  
 CC acute brain injury, acute spinal cord injury, nervous system tumours,  
 CC multiple sclerosis, or infection, haematopoietic cell degeneration or  
 CC insufficiency resulting from eosinopenia, anaemia, thrombocytopenia, or  
 CC stem-cell insufficiencies, cardiac muscle degeneration or insufficiency  
 CC resulting from cardiomyopathy or congestive heart failure. They can also  
 CC be used for treating e.g. peripheral nerve trauma or injury, exposure to  
 CC neurotoxins, metabolic diseases such as diabetes or renal dysfunctions

CC and damage caused by infectious agents. The GP can also be used for  
CC promoting the growth and/or differentiation of a cell in a culture  
CC medium. The antisense polynucleotides can be used for treating a disease  
CC condition mediated by expression of perlepin by a population of cells.  
CC The products can also be used for detection and diagnosis  
XX

SQ Sequence 98 AA;

Query Match 100.0%; Score 96; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGPPYIWSL 15  
|||  
Db 26 HANFCLGPPYIWSL 40

Search completed: June 14, 2005, 15:46:23  
Job time : 88.9615 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 14, 2005, 15:34:23 ; Search time 80.1923 Seconds  
(without alignments)  
95.785 Million cell updates/sec

Title: US-09-831-253F-1  
Perfect score: 96  
Sequence: 1 HANFLGCPFYWSL 15

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	96	100.0	50 2 Q28240	Q28240 cervus elap
2	96	100.0	51 2 Q72487	Q72487 homo sapien
3	96	100.0	78 2 Q70316	Q70316 sus scrofa
4	96	100.0	101 2 Q9R184	Q9R184 meriones un
5	96	100.0	112 2 O02730	O02730 oryctolagus
6	96	100.0	124 2 Q95N80	Q95N80 canis fami1
7	96	100.0	130 2 Q08714	Q08714 mesocricetu
8	96	100.0	315 1 TGF1_BOVIN	P18341 bos taurus
9	96	100.0	368 2 Q8R4D9	Q8R4D9 sigmodon hi
10	96	100.0	390 1 TGF1_CANFA	P54831 canis fami1
11	96	100.0	390 1 TGF1_CAVPO	Q941Y6 cavia porce
12	96	100.0	390 1 TGF1_CERAE	P09533 cercopithec
13	96	100.0	390 1 TGF1_HORSE	O19011 equus caball
14	96	100.0	390 1 TGF1_HUMAN	P01137 homo sapien
15	96	100.0	390 1 TGF1_MOUSE	P04202 mus musculu
16	96	100.0	390 1 TGF1_MOUSE	P07200 mus musculu
17	96	100.0	390 1 TGF1_PIG	P17246 rattus norv
18	96	100.0	390 1 TGF1_RAT	P50414 ovis aries
19	96	100.0	390 2 Q9TUM8	Q9TUM8 equus caball
20	82	85.4	373 1 TGF1_CHICK	P09531 gallus gall
21	77	80.2	412 1 TGF2_CHICK	P30371 gallus gall
22	74	77.1	382 1 TGF1_XENLA	P16176 xenopus lae
23	70	72.9	77 2 Q90YF8	Q90YF8 oncorhynch
24	70	72.9	86 2 Q28241	Q28241 cervus elap
25	70	72.9	88 2 Q90YF7	Q90YF7 oncorhynch
26	70	72.9	91 2 Q9MYZ1	Q9MYZ1 capra hircu
27	70	72.9	112 1 TGF2_BOVIN	P21214 bos taurus
28	70	72.9	224 2 Q8CDZ9	Q8CDZ9 mus musculu
29	70	72.9	255 2 Q921T1	Q921T1 mus musculu
30	70	72.9	361 2 Q98854	Q98854 cyprinus ca
31	70	72.9	399 2 Q9ERB7	Q9ERB7 mesocricetu

32	70	72.9	410 2 Q66123	Q66123 brachydanio
33	70	72.9	410 2 Q7SZV3	Q7SZV3 brachydanio
34	70	72.9	411 2 Q7SZV4	Q7SZV4 brachydanio
35	70	72.9	413 1 TGF2_XENLA	P17247 xenopus lae
36	70	72.9	414 1 TGF2_CERAE	P61811 cercopithec
37	70	72.9	414 1 TGF2_HUMAN	P61812 homo sapien
38	70	72.9	414 1 TGF2_MOUSE	P27090 mus musculu
39	70	72.9	414 2 Q91VP5	Q91VP5 mus musculu
40	70	72.9	435 1 TGF2_PIG	P09858 sus scrofa
41	70	72.9	442 1 TGF2_RAT	Q07257 rattus norv
42	70	72.9	442 2 Q6T7C3	Q6T7C3 oryctolagus
43	69	71.9	62 2 Q90YF4	Q90YF4 pleuronecte
44	68	70.8	62 2 Q90ZJ7	Q90ZJ7 anguilla an
45	68	70.8	62 2 Q9DEP5	Q9DEP5 scophthalmu

## ALIGNMENTS

RESULT 1  
Q28240 PRELIMINARY; PRT; 50 AA.  
AC Q28240;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Transforming growth factor beta 1 (TGF-beta 1) (Transforming growth factor B1) (Fragment).  
GN Name=TGFBI; Synonyms=TGF beta-1, TGF-B1;  
OS Cervus elaphus (Red deer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;  
OC Cervinae; Cervus.  
OX NCBI\_TaxID=9660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Antler;  
RX MEDLINE=98233260; PubMed=9571767;  
RA DOI=10.1002/(SICI)1097-010X(19980501)281:1<36::AID-JE26>3.0.CO;2-D;  
RA Francis S.M., Suttie J.M.;  
RT "Detection of growth factors and proto-oncogene mRNA in the growing tip of red deer (Cervus elaphus) antler using reverse-transcriptase RT polymerase chain reaction (RT-PCR).";  
RL J. Exp. Zool. 281:36-42(1998).  
[2]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Wagener A., Bliotner S., Pickel J.;  
RT "Detection of growth factors in the testes of roe deer (Capreolus capreolus).";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DEPRESSANTS A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.  
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
CC -!- SIMILARITY: Belongs to the TGF-beta family.  
DR EMBL; U62110; AB05256.1; -.  
DR EMBL; AF152591; AAF73230.1; -.  
DR HSSP; P01137; IRLA.  
DR GO; GO:0008083; F: growth factor activity; IEA.  
DR GO; GO:0008283; F: cell proliferation; IEA.  
DR GO; GO:0000074; P: regulation of cell cycle; IEA.  
DR InterPro; IPR001839; TGFb.  
DR Pfam; PF00019; TGF beta; 1.  
DR ProDom; PD000357; TGFb; 1.  
DR SMART; SM00204; TGFb; 1.  
DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
KW Glycoprotein; Growth factor; Mitogen.  
FT NON\_TER 1  
FT CHAIN 1  
FT <1 >50 TRANSFORMING GROWTH FACTOR BETA 1.

[illegible]

DR	GO; GO:008083; F:growth factor activity; IEA.
DR	InterPro; IPRO01839; TGFb.
DR	Pfam; PF00019; TGF_beta; 1.
DR	PRODOM; PD000357; TGFb; 1.
DR	SMART; SM00204; TGFb; 1.
DR	PROSITE; PS00250; TGF_BETA_1; 1.
KW	Growth factor.
FT	NON TER
FT	CHAIN
FT	NON TER
FT	SEQUENCE
SQ	SEQUENCE
Query Match	100.0%; Score 96; DB 2; Length 78;
Best Local Similarity	100.0%; Pred. No. 3.4e-07;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	24 HANFCLGCPYIMSL 38
Oy	1 HANFCLGCPYIMSL 15
ID	Q9R184 PRELIMINARY; PRT; 101 AA.
AC	Q9R184
DT	01-MAY-2000 (TReMBLrel. 13, Created)
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT	01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE	Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN	Name=TGFb1; Synonyms=TGF-BETA;
OS	Meliones ungulicatus (Mongolian jird) (Mongolian gerbil).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OX	NCBI_TaxID=10047;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LMPH NODE;
RA	Rao U.R., Kiet T.R.;
RT	"cDNA cloning of gerbil transforming growth factor-beta by PCR";
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC	-1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC	-1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR	EMBL; AF161218; AAA45726.1; -.
DR	HSSP; P01137; IKA.
DR	GO; GO:008083; F:growth factor activity; IEA.
DR	GO; GO:008283; P:cell proliferation; IEA.
DR	GO; GO:000074; P:regulation of cell cycle; IEA.
DR	InterPro; IPRO01839; TGFb
DR	Pfam; PF00019; TGF_beta; 1.
DR	PRODOM; PD000357; TGFb; 1.
DR	SMART; SM00204; TGFb; 1.
DR	PROSITE; PS00250; TGF_BETA_1; 1.
KW	Glycoprotein; Growth Factor; Mitogen.
FT	NON TER
FT	CHAIN
FT	NON TER
FT	DISULFD
FT	DISULFD
FT	NON TER
SQ	SEQUENCE
Query Match	100.0%; Score 96; DB 2; Length 101;
Best Local Similarity	100.0%; Pred. No. 4.3e-07;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 HANFCLGCPYIMSL 15

Db 34 HANFCLGCPYIWSL 48

# RESULT 5

002730 PRELIMINARY; PRT; 112 AA.  
 AC 002730; 097501;  
 DT 01-JUN-1997 (TREMBlrel. 04, Created)  
 DT 01-JUN-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).  
 GN Name=TGFBI; Synonyms=TGF-beta-1;  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OC NCI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Taylor T.K., James E.R., McGonigle S., Yoho E.R.;  
 RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 2-99 FROM N.A.  
 RA Inoue K., Kawabe Y., Kodama T.;  
 RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS  
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL  
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF  
 CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1  
 CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND  
 CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.

DR EMBL; AF000133; AAB53806.1; -;  
 DR EMBL; AB020217; BAA36950.1; -;  
 DR HSSP; P01137; 1KLA.  
 DR GO; GO:0008083; F:growth factor activity; IEA.  
 DR GO; GO:0008283; P:cell proliferation; IEA.  
 DR GO; GO:000074; P:regulation of cell cycle; IEA.  
 DR InterPro; IPR002400; GF\_cyknct.  
 DR InterPro; IPR001839; TGFb.  
 DR Pfam; PF00019; TGF\_beta; 1.  
 DR PRINTS; PR00438; GFCYSKNOT.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFBI; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Glycoprotein; Growth factor; Mitogen.  
 FT CHAIN 1 112 TRANSFORMING GROWTH FACTOR BETA 1.  
 FT NON\_TER 1 1  
 FT DISULFID 7 16 BY SIMILARITY.  
 FT DISULFID 15 78 BY SIMILARITY.  
 FT DISULFID 44 109 BY SIMILARITY.  
 FT DISULFID 48 111 BY SIMILARITY.  
 FT DISULFID 77 77 INTERCHAIN (BY SIMILARITY).  
 FT CONFLICT 2 3 LD -> FS (IN REF. 2).  
 FT CONFLICT 85 92 PLPTIYIV -> ATAHRYTTL (IN REF. 2).  
 SQ SEQUENCE 112 AA; 12795 MW; 535CB7D46355A6F3 CRC64;

Query Match 100.0%; Score 96; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 4,7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HANFCLGCPYIWSL 54

RESULT 6  
 Q95N80 PRELIMINARY; PRT; 124 AA.  
 ID Q95N80;  
 AC Q95N80;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Transforming growth factor beta 1 (Fragment).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OC NCI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Fontana S., Groene A., Baumgaertner W.;  
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.

DR EMBL; AF349538; AAK54072.1; -;  
 DR HSSP; P01137; 1KLA.  
 DR GO; GO:0008083; F:growth factor activity; IEA.  
 DR InterPro; IPR001839; TGFb.  
 DR Pfam; PF00019; TGF\_beta; 1.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFBI; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Growth factor.  
 FT NON\_TER 1 1  
 FT NON\_TER 124 124  
 SQ SEQUENCE 124 AA; 14329 MW; 21D185218E5556DB CRC64;

Query Match 100.0%; Score 96; DB 2; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15  
 Db 55 HANFCLGCPYIWSL 69

RESULT 7  
 Q08714 PRELIMINARY; PRT; 130 AA.  
 ID Q08714; 070331;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).  
 GN Name=TGFBI;  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OC NCI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=LANG (SYR);  
 RC MEDLINE=93304479; PubMed=8317544;  
 RX Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N.,  
 RA Elvovic A., McBride J., Gallagher G., Todd R.;  
 RT "Sequential expression of transforming growth factors alpha and beta 1  
 RT by eosinophils during cutaneous wound healing in the hamster.";  
 RL Am. J. Pathol. 143:130-142(1993).  
 RN [2]  
 RP SEQUENCE OF 26-115 FROM N.A.  
 RC STRAIN=SYRIAN; TISSUE=SPLEEN;  
 RX MEDLINE=98234044; PubMed=9573100;  
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;  
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and  
 RT analysis of cytokine mRNA expression in experimental visceral  
 RT leishmaniasis.";  
 RL Infect. Immun. 66:2135-2142(1998).  
 CC -1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS  
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL  
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF  
 CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1  
 CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND  
 CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.  
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.  
 CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.

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DR EMBL; X60296; CAA42838.1; -.
DR EMBL; AF046214; AAC40099.1; -.
DR PIR; I48196; I48196.
DR HSSP; P01137; IKLA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR GO; GO:0008283; P: cell proliferation; IEA.
DR GO; GO:0000074; P: regulation of cell cycle; IEA.
DR InterPro; IPR01839; TGFb.
DR Pfam; PF00019; TGF beta; 1.
DR Prodom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Glycoprotein; Growth factor; Mitogen.
FT PROPEP <1 18 TRANSFORMING GROWTH FACTOR BETA 1.
FT CHAIN 19 130 BY SIMILARITY.
FT DISULFID 25 34 BY SIMILARITY.
FT DISULFID 33 96 BY SIMILARITY.
FT DISULFID 66 129 BY SIMILARITY.
FT DISULFID 95 95 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 93 93 G -> S (IN REF. 2).
SQ SEQUENCE 130 AA; 14997 MW; 8B41DD6CF39CA77 CRC64;

Query Match 100.0%; Score 96; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYTWSL 15
DB 58 HANFCLGPCPYTWSL 72

RESULT 8
TGFI_BOVIN STANDARD; PRT; 315 AA.
ID TGFI_BOVIN
AC P18341;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).
GN Name=TGFb1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91042552; PubMed=3153459;
RA van Obberghen-Schilling E., Kondalah P., Ludwig R.L., Sporn M.B.,
RA Baker C.C.;
RT "Complementary deoxyribonucleic acid cloning of bovine transforming
RT growth factor-beta 1."
RL Mcl. Endocrinol. 1:693-698 (1987).
RN [2]
RP SUBUNIT.
RC TISSUE=Bone;
RX MEDLINE=92129307; PubMed=1733936;
RA Ogawa Y., Schmidt D.K., Daech J.R., Chang R.J., Glaser C.B.;
RT "Purification and characterization of transforming growth factor-beta
RT 2.3 and -beta 1.2 heterodimers from bovine bone."
RL J. Biol. Chem. 267:2325-2328 (1992).
DE FUNCTION: TGF-beta is a multifunctional peptide that control
CC proliferation, differentiation, and other functions in many cell
CC types. Many cells synthesize TGF-beta and essentially all of them
CC have specific receptors for this peptide. TGF-beta regulates the
CC actions of many other peptide growth factors and determines a
CC positive or negative direction of their effects. Play an important
CC role in bone remodelling. It is a potent stimulator of
CC osteoblastic bone formation, causing chemotaxis, proliferation and
CC differentiation in committed osteoblasts (by similarity).
CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
CC covalently linked to a latency-associated peptide (LAP) homodimer.

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CC The inactive complex can contain a latent TGF-beta binding protein
CC (by similarity). The active form is a homodimer of mature TGF-beta
CC 1; disulfide-linked. Heterodimers of TGF-beta 1/2 have been found
CC in bone.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
CC and LAP (by similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; M36271; AAA30778.1; -.
DR PIR; A40057; A40057.
DR HSSP; P01137; IKLA.
DR InterPro; IPR002400; GF_Cybknot.
DR InterPro; IPR003911; TGF_TGFb.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR01423; TGFb_BETA.
DR Prodom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Glycoprotein; Growth factor; Mitogen.
FT PROPEP <1 203
FT CHAIN 204 315 Transforming growth factor beta 1.
FT DISULFID 210 219 By similarity.
FT DISULFID 218 281 By similarity.
FT DISULFID 247 312 By similarity.
FT DISULFID 251 314 By similarity.
FT DISULFID 280 280 Interchain (by similarity).
FT CARBOHYD 7 7 N-linked (GlcNAc...) (by similarity).
FT CARBOHYD 61 61 N-linked (GlcNAc...) (by similarity).
FT CARBOHYD 101 101 N-linked (GlcNAc...) (by similarity).
FT SITE 169 171 Cell attachment site (Potential).
SQ SEQUENCE 315 AA; 36269 MW; C2717A23D994E008 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGPCPYTWSL 15
DB 243 HANFCLGPCPYTWSL 257

RESULT 9
Q8R4D9 PRELIMINARY; PRT; 368 AA.
ID Q8R4D9
AC Q8R4D9;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Transforming growth factor beta-1 protein (Fragment).
GN Name=Tgfb1;
OS Simodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OC NCBI_Taxid=42415;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14980081; DOI=10.1089/107999004772719873;
RA Blanco J.C., Pletneva L., Boukhalova M., Richardson J.Y.,

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RA Harris K.A., Prince G.A.;  
 RT "The cotton rat: an underutilized animal model for human infectious  
 RT diseases can now be exploited using specific reagents to cytokines,  
 RT chemokines, and interferons";  
 RL J. Interleukin Cytochrome Res. 24:21-28(2004).  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.  
 DR EMBL; AF480858; AAL87199.1; -.  
 DR HSSP; P01137; IKLA.  
 DR GO; GO:0008063; F:transforming growth factor beta receptor bi. . .; IEA.  
 DR GO; GO:0005160; F:transforming growth factor beta receptor bi. . .; IEA.  
 DR GO; GO:0016049; P:cell growth; IEA.  
 DR InterPro; IPR002400; GF\_cysknob.  
 DR InterPro; IPR001839; TGFb.  
 DR InterPro; IPR003939; TGFb.N.  
 DR InterPro; IPR001111; TGFb.N.  
 DR InterPro; IPR003911; TGF\_TGFb.  
 DR Pfam; PF00688; TGFb\_propeptide; 1.  
 DR Pfam; PF00019; TGF\_beta; 1.  
 DR PRINTS; PRO0438; GFCYSKNOT.  
 DR PRINTS; PRO1423; TGFbeta.  
 DR PRINTS; PRO1424; TGFbeta1.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 DR Growth factor.  
 FT NON TER  
 SQ SEQUENCE 368 AA; 41905 MW; A5C91207B0468B4A CRC64;  
 Query Match 100.0%; Score 96; DB 2; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15  
 DB 296 HANFCLGCPYIWSL 310

RESULT 10  
 TGFL\_CANFA STANDARD; PRT; 390 AA.  
 AC PS4831;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
 GN Name=TGFb1;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Jugular vein endothelial;  
 RX MEDLINE=95237630; PubMed=7721110; DOI=10.1016/0378-1119(94)00903-6;  
 RA Manning A.M., Auchampach J.A., Drong R.F., Slichter J.L.;  
 RT "Cloning of a canine cDNA homologous to the human transforming growth  
 RT factor-beta 1-encoding gene";  
 RU Gene 155:307-308(1995).  
 CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control  
 CC proliferation, differentiation, and other functions in many cell  
 CC types. Many cells synthesize TGF-beta and essentially all of them  
 CC have specific receptors for this peptide. TGF-beta regulates the  
 CC actions of many other peptide growth factors and determines a  
 CC positive or negative direction of their effects. Play an important  
 CC role in bone remodeling. It is a potent stimulator of  
 CC osteoblastic bone formation, causing chemotaxis, proliferation and  
 CC differentiation in committed osteoblasts (By similarity).  
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
 CC covalently linked to a latency-associated peptide (LAP) homodimer.  
 CC The inactive complex can contain a latent TGF-beta binding  
 CC protein. The active form is a homodimer of mature TGF-beta 1;  
 CC disulfide-linked (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
 CC and LAP (By similarity).  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.  
 CC -----  
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 CC -----  
 DR EMBL; L34956; AAA51458.1; -.  
 DR PIR; JC4023; JC4023.  
 DR HSSP; P01137; IKLA.  
 DR InterPro; IPR002400; GF\_cysknob.  
 DR InterPro; IPR003911; TGF\_TGFb.  
 DR InterPro; IPR001839; TGFb.  
 DR InterPro; IPR001111; TGFb.N.  
 DR Pfam; PF00019; TGF\_beta; 1.  
 DR Pfam; PF00688; TGFb\_propeptide; 1.  
 DR PRINTS; PRO0438; GFCYSKNOT.  
 DR PRINTS; PRO1423; TGFbeta.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 DR Glycoprotein; Growth factor; Mitogen; Signal.  
 FT SIGNAL 1 29  
 FT PROPEP 30 278  
 FT CHAIN 279 390  
 FT DISULFID 285 294  
 FT DISULFID 293 356  
 FT DISULFID 322 387  
 FT DISULFID 326 389  
 FT DISULFID 355 355  
 FT CARBOHYD 82 85  
 FT CARBOHYD 136 136  
 FT CARBOHYD 176 176  
 FT SITE 244 246  
 SQ SEQUENCE 390 AA; 44185 MW; EB4780EB8B7B5908 CRC64;  
 Query Match 100.0%; Score 96; DB 1; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15  
 DB 318 HANFCLGCPYIWSL 332

RESULT 11  
 TGFL\_CANFO STANDARD; PRT; 390 AA.  
 AC Q921Y6; Q9Q2H3; Q9R148;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
 GN Name=TGFb1;  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Hartley;  
 RA Jeevan A., McMurray D.N., Yoshimura T.;  
 RT "Guinea pig transforming growth factor-beta in peritoneal exudates  
 RT after BCG vaccination";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 265-382 FROM N.A.



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DR EMBL; M16658; AAA5369.1; -

DR PIR; A26960; A26960.

DR HSSP; P01137; 1KLA.

DR InterPro; IPR002400; GF\_cysknot.

DR InterPro; IPR003911; TGF\_TGFB.

DR InterPro; IPR001839; TGFB.

DR InterPro; IPR001111; TGFB.N.

DR Pfam; PF00019; TGF\_beta.1.

DR Pfam; PF00688; TGFB\_propeptide.1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PRINTS; PR01423; TGFBETA.

DR ProDom; PD000357; TGFB.1.

DR SMART; SM00204; TGFB.1.

DR PROSITE; PS00250; TGF\_BETA\_1; 1.

DR Glycoprotein; Growth Factor; Mitogen; Signal.

FT SIGNAL 1 29

FT PROPEP 30 278 Latency-associated peptide.

FT CHAIN 279 390 Transforming growth factor beta 1.

FT DISULFID 285 294 By similarity.

FT DISULFID 293 356 By similarity.

FT DISULFID 322 387 By similarity.

FT DISULFID 326 389 By similarity.

FT DISULFID 355 355 Interchain (By similarity).

FT CARBOHYD 82 82 N-linked (GlcNAc...).

FT CARBOHYD 136 136 N-linked (GlcNAc...).

FT CARBOHYD 176 176 N-linked (GlcNAc...).

FT SITE 244 246 Cell attachment site (Potential).

FT SEQUENCE 390 AA; 44356 MW; DPF63B2BAB44320E CRC64;

Query Match 100.0%; Score 96; DB 1; Length 390;

Best Local Similarity 100.0%; Pred. No. 1.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGPCPYMSL 15

Db 318 HANFCLGPCPYMSL 332

RESULT 13

TGFL\_HORSE STANDARD; PRT; 390 AA.

AC O19011;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Transforming growth factor beta 1 precursor (TGF-beta 1).

GN Name=TGFB1;

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI\_TaxID=9796;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph node;

RA MEDLINE=96185507; PubMed=9524819;

RA Pechla-Gonzales M.N., Onions D.E., Nicolson L.,

RT "Cloning and sequencing of equine transforming growth factor-beta 1 (TGF-beta-1) cDNA."

RL DNA Seq. 7:375-378(1997).

-1- FUNCTION: TGF-beta is a multifunctional peptide that control proliferation, differentiation, and other functions in many cell types. Many cells synthesize TGF-beta and essentially all of them have specific receptors for this peptide. TGF-beta regulates the actions of many other peptide growth factors and determines positive or negative direction of their effects. Play an important role in bone remodelling. It is a potent stimulator of osteoblastic bone formation, causing chemotaxis, proliferation and differentiation in committed osteoblasts (By similarity).

-1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-covalently linked to a latency-associated peptide (LAP) homodimer.

The inactive complex can contain a latent TGF-beta binding protein. The active form is a homodimer of mature TGF-beta 1; disulfide-linked (By similarity).

-----

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1 and LAP (By similarity).

CC -1- SIMILARITY: Belongs to the TGF-beta family.

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-----

DR EMBL; X99438; CAA67801.1; -

DR HSSP; P01137; 1KLA.

DR InterPro; IPR002400; GF\_cysknot.

DR InterPro; IPR003911; TGF\_TGFB.

DR InterPro; IPR001839; TGFB.

DR InterPro; IPR001111; TGFB.N.

DR Pfam; PF00019; TGF\_beta.1.

DR Pfam; PF00688; TGFB\_propeptide.1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PRINTS; PR01423; TGFBETA.

DR ProDom; PD000357; TGFB.1.

DR SMART; SM00204; TGFB.1.

DR PROSITE; PS00250; TGF\_BETA\_1; 1.

DR Glycoprotein; Growth Factor; Mitogen; Signal.

FT SIGNAL 1 29

FT PROPEP 30 278 Latency-associated peptide (By similarity).

FT CHAIN 279 390 Transforming growth factor beta 1.

FT DISULFID 285 294 By similarity.

FT DISULFID 293 356 By similarity.

FT DISULFID 322 387 By similarity.

FT DISULFID 326 389 By similarity.

FT DISULFID 355 355 Interchain (By similarity).

FT CARBOHYD 82 82 N-linked (GlcNAc...).

FT CARBOHYD 136 136 N-linked (GlcNAc...).

FT CARBOHYD 176 176 N-linked (GlcNAc...).

FT SEQUENCE 390 AA; 43974 MW; A86D715F44549691 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 390;

Best Local Similarity 100.0%; Pred. No. 1.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGPCPYMSL 15

Db 318 HANFCLGPCPYMSL 332

RESULT 14

TGFL\_HUMAN STANDARD; PRT; 390 AA.

AC P01137; Q9UCG4;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Transforming growth factor beta 1 precursor (TGF-beta 1).

GN Name=TGFB1; Synonyms=TGFB;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=87174845; PubMed=3470709;

RX Derynck R., Rhee L., Chen E.Y., van Tilburg A.;

RA "Intron-exon structure of the human transforming growth factor-beta 1 precursor gene."

RL Nucleic Acids Res. 15:3188-3189(1987).

[2]  
 RN SEQUENCE FROM N.A., AND VARIANT PRO-10.  
 RX MEDLINE=85296301; PubMed=3861940;  
 RA Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,  
 RA Assoian R.K., Roberts A.B., Sporn M.B., Goeddel D.V.,  
 RT "Human transforming growth factor-beta complementary DNA sequence and  
 RT expression in normal and transformed cells.";  
 RL Nature 316:701-705(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ductodenum, and Eye;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubenberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP SEQUENCE OF 279-390 FROM N.A.  
 RC TISSUE=Carcinoma;  
 RX MEDLINE=93229900; PubMed=8471846; DOI=10.1006/prep.1993.1019;  
 RA Bourdel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugarman B.J.,  
 RA Hu S., Westcott K.R.,  
 RT "Recombinant human transforming growth factor-beta 1: expression by  
 RT Chinese hamster ovary cells, isolation, and characterization.";  
 RL Protein Expr. Purif. 4:130-140(1993).  
 RN [6]  
 RP SEQUENCE OF 279-301.  
 RX MEDLINE=85131019; PubMed=2982829;  
 RA Massague J., Like B.,  
 RT "Cellular receptors for type beta transforming growth factor. Ligand  
 RT binding and affinity labeling in human and rodent cell lines.";  
 RL J. Biol. Chem. 260:2636-2645(1985).  
 RN [7]  
 RP SEQUENCE OF 30-42 AND 279-290, AND CHARACTERIZATION.  
 RX PubMed=3162913;  
 RA Miyazono K., Hellman U., Wernstedt C., Heldin C.H.,  
 RT "Latent high molecular weight complex of transforming growth factor  
 RT beta 1. Purification from human platelets and structural  
 RT characterization.";  
 RL J. Biol. Chem. 263:6407-6415(1988).  
 RN [8]  
 RP REVIEW.  
 RX PubMed=9150447;  
 RA Munger J.S., Harpel J.G., Gleizes P.E., Mazziari R., Nunes I.,  
 RA Rifkin B.B.,  
 RT "Latent transforming growth factor-beta: structural features and  
 RT mechanisms of activation.";  
 RL Kidney Int. 51:1376-1382(1997).  
 RN [9]  
 RP  
 RP STRUCTURE BY NMR OF 279-390.  
 RX MEDLINE=93144319; PubMed=8424942;  
 RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,  
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,  
 RA Torchia D.A.,  
 RT "Transforming growth factor beta 1: NMR signal assignments of the  
 RT recombinant protein expressed and isotopically enriched using Chinese  
 RT hamster ovary cells.";  
 RL Biochemistry 32:1152-1163(1993).  
 RN [10]  
 RP STRUCTURE BY NMR OF 279-390.  
 RX MEDLINE=93144320; PubMed=8424943;  
 RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,  
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,  
 RA Torchia D.A.,  
 RT "Transforming growth factor beta 1: secondary structure as determined  
 RT by heteronuclear magnetic resonance spectroscopy.";  
 RL Biochemistry 32:1164-1171(1993).  
 RN [11]  
 RP STRUCTURE BY NMR OF 279-390.  
 RX MEDLINE=96266150; PubMed=8679613; DOI=10.1021/bi9604946;  
 RA Hick A.P., Archer S.J., Qian S.W., Roberts A.B., Sporn M.B.,  
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,  
 RA Torchia D.A.,  
 RT "Transforming growth factor beta 1: three-dimensional structure in  
 RT solution and comparison with the X-ray structure of transforming  
 RT growth factor beta 2.";  
 RL Biochemistry 35:8517-8534(1996).  
 RN [12]  
 RP TISSUE SPECIFICITY.  
 RX PubMed=11746498; DOI=10.1002/jcb.1249;  
 RA Shur I., Lokiec F., Blalberg I., Benayahu D.,  
 RT "Differential gene expression of cultured human osteoblasts.";  
 RL J. Cell. Biochem. 83:547-553(2001).  
 RN [13]  
 RP VARIANT PRO-10.  
 RX PubMed=9783545;  
 RA Yamada Y., Myauchi A., Goto J., Takagi Y., Okuzumi H., Kanematsu M.,  
 RA Hase M., Takai H., Harada A., Ikeda K.,  
 RT "Association of a polymorphism of the transforming growth factor-beta1  
 RT gene with genetic susceptibility to osteoporosis in postmenopausal  
 RT Japanese women.";  
 RL J. Bone Miner. Res. 13:1569-1576(1998).  
 RN [14]  
 RP VARIANTS CED CVS-218; HIS-218 AND ARG-225.  
 RX PubMed=10973241; DOI=10.1038/79128;  
 RA Kinoshita A., Saito T., Tomita H., Makita Y., Yoshida K., Ghadami M.,  
 RA Yamada K., Kondo S., Ikegawa S., Nishimura G., Fukushima Y.,  
 RA Nakagomi T., Saito H., Sugimoto T., Kamegaya M., Hise K., Murray J.C.,  
 RA Taniguchi N., Nishikawa N., Yoshitake K.,  
 RT "Domain-specific mutations in TGFBI result in Camurati-Engelmann  
 RT disease.";  
 RL Nat. Genet. 26:19-20(2000).  
 RN [15]  
 RP VARIANTS CED HIS-81; CVS-218 AND ARG-225.  
 RX PubMed=11062463; DOI=10.1038/81563;  
 RA Janssens K., Gerschlager R., Guanabens N., Migone N., Ralston S.,  
 RA Bonduelle M., Lissens W., Van Maldergem L., Vanhoenacker F.,  
 RA Verbruggen L., Van Hul W.,  
 RT "Mutations in the gene encoding the latency-associated peptide of TGF-  
 RT beta 1 cause Camurati-Engelmann disease.";  
 RL Nat. Genet. 26:273-275(2000).  
 RN [16]  
 RP VARIANT PRO-10.  
 RX PubMed=12202987; DOI=10.1007/s100380200069;  
 RA Watanabe Y., Kinoshita A., Yamada T., Ohta T., Kishino T.,  
 RA Matsuno N., Ishikawa M., Nishikawa N., Yoshitake K.,  
 RT "A catalog of 106 single-nucleotide polymorphisms (SNPs) and 11 other  
 RT types of variations in genes for transforming growth factor-beta1  
 RT (TGF-beta1) and its signaling pathway.";  
 RL J. Hum. Genet. 47:478-483(2002).  
 RN [17]  
 RP CHARACTERIZATION OF VARIANTS CED HIS-81; CVS-218; ASP-222 AND ARG-225.  
 RX

RX PubMed=12493741; DOI=10.1074/jbc.M208857200;  
RA Janssens K., ten Dijke P., Ralston S.H., Bergmann C., Van Hul W.;  
RT "Transforming growth factor-beta-1 mutations in Camurati-Engelmann  
disease lead to increased signaling by altering either activation or  
secretion of the mutant protein";  
RL J. Biol. Chem. 278:7718-7724(2003).  
RN [18]  
RP CHARACTERIZATION OF VARIANT CVS-218.  
RX PubMed=12843182; DOI=10.1210/jc.2002-020564;  
RA McGowan N.W., Macpherson H., Janssens K., Van Hul W., Firth J.C.,  
RA Fraser W.D., Ralston S.H., Helfrich M.H.;  
RT "A mutation affecting the latency-associated peptide of TGFbeta1 in  
Camurati-Engelmann disease enhances osteoclast formation in vitro";  
RL J. Clin. Endocrinol. Metab. 88:3321-3326(2003).  
CC -1- FUNCTION: Multifunctional peptide that controls proliferation,  
differentiation, and other functions in many cell types. Many  
cells synthesize TGF-beta 1 and essentially all of them have  
specific receptors for this peptide. TGF-beta 1 regulates the  
actions of many other peptide growth factors and determines a  
positive or negative direction of their effects. Play an important  
role in bone remodeling. It is a potent stimulator of  
osteoblastic bone formation, causing chemotaxis, proliferation and  
differentiation in committed osteoblasts (by similarity).  
CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
covalently linked to a latency-associated peptide (LAP) homodimer.  
CC The inactive complex can contain a latent TGF-beta binding  
protein. The active form is a homodimer of mature TGF-beta 1;  
CC disulfide-linked.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Highly expressed in bone.  
CC -1- INDUCTION: Activated in vitro at pH below 3.5 and over 12.5.  
CC -1- PTM: Glycosylated (By similarity). The precursor is cleaved into  
CC mature TGF-beta 1 and LAP.  
CC -1- POLYMORPHISM: In post-menopausal Japanese women, the frequency of  
CC Leu-10 is higher in subjects with osteoporosis than in controls.  
CC -1- DISEASE: Defects in TGFBI are the cause of Camurati-Engelmann  
Query Match 100.0%; Score 96; DB 1; Length 390;  
Best Local Similarity 100.0%; Pred. No. 1,4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HANFCLGPCPYIMSL 15  
Db 318 HANFCLGPCPYIMSL 332  
RESULT 15  
TGF1 MOUSE STANDARD; PRT; 390 AA.  
ID TGF1 MOUSE  
AC P04202;  
DT 20-MAR-1987 (Rel. 04, Created)  
DT 20-MAR-1987 (Rel. 04, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
GN Name=Tgfb1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCB1\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86168129; PubMed=3007454;  
RA Derynck R., Jarrett J.A., Chen E.Y., Goeddel D.V.;  
RT "The murine transforming growth factor-beta precursor";  
RL J. Biol. Chem. 261:4377-4379(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BAJB/c;  
RX MEDLINE=96095545; PubMed=8522200; DOI=10.1016/0378-1119(95)00460-N;  
RA Guron C., Sudarshan C., Raghow R.;  
RT "Molecular organization of the gene encoding murine transforming  
growth factor beta 1";  
RL Gene 165:325-326(1995).

RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6, and NOD/Lt; TISSUE=Spleen;  
RA Poirat L., Benoist C., Mathis D.;  
RT "Transforming growth factor-beta 1 sequence and expression: no  
difference between NOD/Lt and C57BL/6 mouse strains";  
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Mammary gland;  
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrincci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control  
CC proliferation, differentiation, and other functions in many cell  
CC types. Many cells synthesize TGF-beta and essentially all of them  
CC have specific receptors for this peptide. TGF-beta regulates the  
CC actions of many other peptide growth factors and determines a  
CC positive or negative direction of their effects. Play an important  
CC role in bone remodeling. It is a potent stimulator of  
CC osteoblastic bone formation, causing chemotaxis, proliferation and  
CC differentiation in committed osteoblasts (by similarity).  
CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
CC covalently linked to a latency-associated peptide (LAP) homodimer.  
CC The inactive complex can contain a latent TGF-beta binding  
CC protein. The active form is a homodimer of mature TGF-beta 1;  
CC disulfide-linked (by similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
CC and LAP (by similarity).  
CC -1- SIMILARITY: Belongs to the TGF-beta family.  
CC -----  
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CC -----  
DR EMBL; M13177; AAA40423.1; -;  
DR EMBL; L42462; AAB00138.1; -;  
DR EMBL; L42456; AAB00138.1; JOINED.  
DR EMBL; L42457; AAB00138.1; JOINED.  
DR EMBL; L42458; AAB00138.1; JOINED.  
DR EMBL; L42459; AAB00138.1; JOINED.  
DR EMBL; L42460; AAB00138.1; JOINED.  
DR EMBL; L42461; AAB00138.1; JOINED.  
DR EMBL; AJ009862; CAA08900.1; -;  
DR EMBL; BC013738; AAH13738.1; -;  
DR PIR; A01396; WFM52.  
DR HSSP; P01137; IKIA.  
DR MSG; MG1:98725; Tgfb1.  
DR GO; GO:0005578; C:extracellular matrix; IDA.  
DR GO; GO:0006954; P:inflammatory response; IMP.

DR GO; GO:0007515; P:lymph gland development; IMP.  
 DR GO; GO:0008220; P:necrosis; IMP.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.  
 DR GO; GO:0042127; P:regulation of cell proliferation; IDA.  
 DR GO; GO:0016202; P:regulation of myogenesis; IDA.  
 DR GO; GO:0042306; P:regulation of protein-nucleus import; IDA.  
 DR GO; GO:0007179; P:transforming growth factor beta receptor sl. . .; IDA.  
 DR InterPro; IPR002400; GF cyknot.  
 DR InterPro; IPR003911; TGF TGFb.  
 DR InterPro; IPR001839; TGFb.  
 DR InterPro; IPR01111; TGFb.N.  
 DR Pfam; PF00019; TGF\_beta; 1.  
 DR Pfam; PF00688; TGFb\_propeptide; 1.  
 DR PRINTS; PRO0438; GFCYSKNOT.  
 DR PRINTS; PRO1423; TGFbeta.  
 DR Prodom; PD000357; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 DR GlycoProtein; Growth factor; Mitogen; Signal.  
 FT SIGNAL 1 29 By similarity.  
 FT PROPEP 30 278 Latency-associated peptide.  
 FT CHAIN 279 390 Transforming growth factor beta 1.  
 FT DISULFID 285 294 By similarity.  
 FT DISULFID 293 356 By similarity.  
 FT DISULFID 322 387 By similarity.  
 FT DISULFID 326 389 By similarity.  
 FT DISULFID 355 355 Interchain (By similarity).  
 FT CARBOHYD 82 82 N-linked (GlcNAc..)(By similarity).  
 FT CARBOHYD 136 136 N-linked (GlcNAc..)(By similarity).  
 FT CARBOHYD 176 176 N-linked (GlcNAc..)(By similarity).  
 FT SITE 244 246 Cell attachment site (Potential).  
 SQ SEQUENCE 390 AA; 44310 MW; 4381A51B711D689E CRC64;

Query March 100.0%; Score 96; DB 1; Length 390;  
 Best local similarity 100.0%; Pred. NO. 1.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HANFCLGPPYIWSL 15  
 |||||  
 Db 318 HANFCLGPPYIWSL 332

Search completed: June 14, 2005, 15:51:06  
 Job time : 81.1923 secs

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OM protein - protein search, using sw model

Run on: June 14, 2005, 15:35:40 ; Search time 16.7308 Seconds  
(without alignments)  
86.263 Million cell updates/sec

Title: US-09-831-253F-1

Perfect score: 96

Sequence: 1 HANFCLGPCPYTWSL 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: dir1: \*  
2: dir2: \*  
3: dir3: \*  
4: dir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	96	100.0	130	2	148196	transforming growt
2	96	100.0	315	2	A40057	transforming growt
3	96	100.0	390	1	WPHU2	transforming growt
4	96	100.0	390	1	WPM52	transforming growt
5	96	100.0	390	2	A26960	transforming growt
6	96	100.0	390	2	JC4023	transforming growt
7	96	100.0	390	2	A27512	transforming growt
8	96	100.0	390	2	I46463	transforming growt
9	96	100.0	390	2	S10219	transforming growt
10	96	100.0	391	2	S01413	transforming growt
11	82	85.4	373	2	A41918	transforming growt
12	77	80.2	412	2	A39489	transforming growt
13	74	77.1	382	2	B61036	transforming growt
14	70	72.9	413	1	WFXLB2	transforming growt
15	70	72.9	413	1	WFXLB2	transforming growt
16	70	72.9	414	1	WPMKB2	transforming growt
17	70	72.9	414	1	WPMKB2	transforming growt
18	70	72.9	414	2	A31249	transforming growt
19	70	72.9	442	2	B31249	transforming growt
20	64	66.7	409	2	S01825	transforming growt
21	64	66.7	410	2	A41397	transforming growt
22	64	66.7	410	2	A55706	transforming growt
23	64	66.7	412	2	A36169	transforming growt
24	62	64.6	412	2	A34939	transforming growt
25	49	51.0	360	2	A29619	Vgl embryonic growt
26	48	50.0	102	2	A36192	inhibin beta-A cha
27	48	50.0	115	2	PM0504	inhibin beta-A cha
28	48	50.0	424	1	B40905	inhibin beta-A cha
29	48	50.0	424	1	S31440	inhibin beta-A cha

30	48	50.0	424	1	WPGGBA	inhibin beta-A cha
31	48	50.0	425	1	S50898	inhibin beta-A cha
32	48	50.0	425	1	I47072	inhibin beta-A cha
33	48	50.0	426	1	B24248	inhibin beta-A cha
34	48	50.0	768	2	T22758	hypothetical prote
35	46	47.9	108	2	D69017	hypothetical prote
36	46	47.9	864	2	JC4624	alpha-glucosidase
37	44	45.8	352	2	JC2466	inhibin beta-C cha
38	44	45.8	399	2	C71728	probable oxygen-in
39	44	45.8	404	2	AB3473	oxygen-independent
40	44	45.8	593	2	F69885	excitaclease ABC s
41	44	45.8	827	2	S48465	6-phosphofructo-2-
42	44	45.8	1382	1	INHUR	insulin receptor p
43	43.5	45.3	239	2	G02630	FcalphaRb - human
44	43.5	45.3	287	2	JH0332	IGb (Fc) receptor,
45	43	44.8	221	2	T20781	hypothetical prote

## ALIGNMENTS

```
RESULT 1
148196
transforming growth factor beta-1 precursor - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 02-Jul-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C:Accession: 148196
R:Wong, D.T.; Donoff, R.B.; Yang, J.; Song, B.Z.; Matossian, K.; Nagura, N.; Elovic, A.;
Am. J. Pathol. 143, 130-142, 1993
A:Title: Sequential expression of transforming growth factors alpha and beta 1 by eosin
A:Reference number: 148196; MUID:93304479; PMID:8317544
A:Accession: 148196
A>Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-130 <RES>
A:Cross-references: UNIPROT:Q08714; EMBL:X60296; NID:g396177; PIDN:CAA42838.1; PID:g3961
C:Superfamily: inhibin

Query Match      100.0%; Score 96; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 HANFCLGPCPYTWSL 15
Db      58 HANFCLGPCPYTWSL 72

RESULT 2
A40057
transforming growth factor beta-1 precursor - bovine (fragment)
N:Alternate names: beta-TGF; cartilage-inducing factor-A; EGF-dependent TGF or dEGF; MGF
C:Species: Bos primigenius taurus (cattle)
C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
C:Accession: A40057; A42320; A05284; A24322; B61439
R:Van Obberghen-Schilling, E.; Kondalish, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.
Mol. Endocrinol. 1, 693-698, 1987
A:Title: Complementary deoxyribonucleic acid cloning of bovine transforming growth facto
A:Reference number: A40057; MUID:91042552; PMID:3153459
A:Accession: A40057
A:Molecule type: mRNA
A:Residues: 1-315 <VAN>
A:Cross-references: UNIPROT:P18341; GB:M6271; NID:g163747; PIDN:AAA30778.1; PID:g163748
R:Ogawa, Y.; Schmidt, D.K.; Daesch, J.R.; Chang, R.U.; Glaeser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A:Title: Purification and characterization of transforming growth factor-beta2.3 and -be
A:Reference number: A42320; MUID:92129307; PMID:1733936
A:Accession: A42320
A:Molecule type: protein
A:Residues: 204-209, X, 211-217 <OCA>
R:Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan, Y.C.E.; Stei
Biochemistry 22, 5692-5698, 1983
A:Title: Purification and properties of a type beta transforming growth factor from bovi
A:Reference number: A05284; MUID:84104793; PMID:6607069
```

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A:Accession: A05284
A:Molecule type: protein
A:Residues: 204-218 <ROB>
R:Sejedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti, A.; Sid
U. Biol. Chem. 261, 5693-5695, 1986
A:Title: Cartilage-inducing factor-A. Apparent identity to transforming growth factor-be
A:Reference number: A24322; MUID:86195954; PMID:375555
A:Accession: A24322
A:Molecule type: protein
A:Residues: 204-233 <SEV>
R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
U. Protein Chem. 10, 565-575, 1991
A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta
A:Reference number: A61439; MUID:92189724; PMID:1799413
A:Accession: B61439
A:Molecule type: protein
A:Residues: 204-209, 'X', 211-217, 'XX', 220-232 <JIN>
C:Comment: This polypeptide is composed of two polypeptide chains cross-linked by disulf
C:Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogenic a
ion. Cells grown in monolayer do not respond in a similar manner to these growth factors
C:Superfamily: inhibin
C:Keywords: glycoprotein; growth factor; heterodimer
F:204-315/Product: transforming growth factor beta-1 #status experimental <MAT>
F:7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          100.0%; Score 96; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 HANFCLGCPYIMSL 15
DB      243 HANFCLGCPYIMSL 257

RESULT 3
WFMU2
transforming growth factor beta-1 precursor [validated] - human
N:Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1986 #sequence revision 19-Oct-1995 #text_change 09-Jul-2004
A:Accession: A27513; A01395; A22290; I59664; S53444
R:Derynck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.
Nucleic Acids Res. 15, 3188-3189, 1987
A:Title: Intron-exon structure of the human transforming growth factor-beta precursor ge
A:Reference number: A27513; MUID:87174845; PMID:3470709
A:Accession: A27513
A:Molecule type: DNA
A:Residues: 1-390 <DER>
A:Cross-references: UNIPROT:P01137; GB:X05839; GB:Y00112; NID:937097; PID:CAA29283.1; F
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assoian, R.K.; Robert
Nature 316, 701-705, 1985
A:Title: Human transforming growth factor-beta complementary DNA sequence and expression
A:Reference number: A01395; MUID:85296501; PMID:3861940
A:Accession: A01395
A:Molecule type: mRNA
A:Residues: 1-9, 'P', 11-24, 'P', 26-159, 'R', 160-390 <DER>
A:Cross-references: GB:X02812; GB:Y05114; NID:937092; PID:CAA26580.1; PID:937093
A:Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a
R:Massague, J.; Ilike, B.
U. Biol. Chem. 260, 2636-2645, 1985
A:Title: Cellular receptors for type beta transforming growth factor. Ligand binding and
A:Reference number: A22290; MUID:85131019; PMID:2982829
A:Accession: A22290
A:Molecule type: protein
A:Residues: 279-285, 'XX', 298-301 <MAS>
R:Urushizaki, Y.; Nitsun, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.; Urushizaki,
Tumor Res. 22, 41-55, 1987
A:Title: Cloning and expression of the gene for human transforming growth factor-beta in
A:Reference number: I59664
A:Accession: I59664
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 279-390 <RES>

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A:Cross-references: GB:M38449; NID:9339557; PID:AAA36735.1; PID:9339558
R:Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyo, D.; Chait, B.T.; Marshak, D.R.,
Biochem. J. 305, 87-92, 1995
A:Title: Physical and biological characterization of a growth-inhibitory activity purified
A:Reference number: S53444; MUID:95126934; PMID:7826358
A:Accession: S53444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 279-297 <STA>
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
C:Genetic:
A:Gene: GDB:TCFBL1, TCFB
A:Cross-references: GDB:120729; OMIM:190180
A:Map position: 19q13.2-19q13.2
C:Superfamily: inhibin
C:Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-278/Domain: propeptide #status predicted <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          100.0%; Score 96; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 HANFCLGCPYIMSL 15
DB      318 HANFCLGCPYIMSL 332

RESULT 4
WFM52
transforming growth factor beta-1 precursor - mouse
N:Alternate names: TGF type 2; TGF-beta
C:Species: Mus musculus (house mouse)
C:Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text_change 09-Jul-2004
A:Accession: A01396
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.
U. Biol. Chem. 261, 4377-4379, 1986
A:Title: The murine transforming growth factor-beta precursor.
A:Reference number: A01396; MUID:86168129; PMID:3007454
A:Accession: A01396
A:Molecule type: mRNA
A:Residues: 1-390 <DER>
A:Cross-references: UNIPROT:P04202; GB:M13177; NID:9201952; PID:AAA40423.1; PID:9201953
A:Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
C:Superfamily: inhibin
C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen; transform
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-278/Domain: propeptide #status predicted <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          100.0%; Score 96; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 HANFCLGCPYIMSL 15
DB      318 HANFCLGCPYIMSL 332

RESULT 5
A26960
transforming growth factor beta-1 precursor - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text_change 09-Jul-2004
A:Accession: A26960
R:Sharples, K.; Ploorman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
DNA 6, 239-244, 1987

```



A>Title: Cloning and sequence analysis of simian transforming growth factor-beta cDNA.  
A:Reference number: A26960; MUID:87246074; PMID:3474130  
A:Accession: A26960  
A:Molecule type: mRNA  
A:Residues: 1-390 <SHA>  
A:Cross-references: UNIPROT:P09533; GB:M16658; NID:G176552; PIDN:AAA35369.1; PID:G176553  
A:Molecule type: mRNA  
A:Superfamily: inhibin  
C:Keywords: growth factor  
F:1-16/Domain: signal sequence  
F:17-390/Product: transforming growth factor beta  
#status predicted <SIG>  
#status predicted <MAT>

Query Match 100.0%; Score 96; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15  
|||||  
Db 318 HANFCLGCPYIWSL 332

## RESULT 6

transforming growth factor beta-1 - dog  
C/Species: Canis lupus familiaris (dog)  
C/Date: 13-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 09-Jul-2004  
A:Accession: J04023  
R:Manning, A.M.; Auchampach, J.A.; Drony, R.F.; Slightom, J.L.  
Gene 150, 307-308, 1995

A>Title: Cloning of a canine cDNA homologous to the human transforming growth factor-beta  
A:Reference number: J04023; MUID:95237630; PMID:7721110  
A:Accession: J04023  
A:Molecule type: mRNA

A:Residues: 1-390 <MAN>  
A:Cross-references: UNIPROT:P54831; GB:IJ34956; NID:G516071; PIDN:AAA51458.1; PID:G516072  
A:Comment: This factor plays a multifunctional role as a regulator of mammalian cell growth

C/Genetics:  
A:Gene: tgf-beta1  
C:Superfamily: inhibin

C:Keywords: growth factor; transforming protein  
F:28-350/Product: transforming growth factor beta 1 #status predicted <MAT>

Query Match 100.0%; Score 96; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15  
|||||  
Db 318 HANFCLGCPYIWSL 332

## RESULT 7

transforming growth factor beta-1 precursor - pig  
N/Alternate names: TGF-beta

C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 09-Jul-2004  
A:Accession: A27512; A26356; I46537  
R:Derynck, R.; Rhee, L.

Nucleic Acids Res. 15, 3187, 1987  
A>Title: Sequence of the porcine transforming growth factor-beta precursor.  
A:Reference number: A27512; MUID:87174844; PMID:3470708

A:Accession: A27512  
A:Molecule type: mRNA  
A:Residues: 1-390 <DER>

A:Cross-references: UNIPROT:P07200  
R:Chelifeitz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.B.; Lucae, R.;  
Cell 48, 409-415, 1987

A>Title: The transforming growth factor-beta system, a complex pattern of cross-reactive  
A:Reference number: A30830; MUID:87102890; PMID:2879635  
A:Accession: A26356  
A:Molecule type: protein

A:Residues: 279-322 <CHE>  
R:Kondatiah, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn, M.B.; Robert

J. Biol. Chem. 263, 18313-18317, 1988

A>Title: cDNA cloning of porcine transforming growth factor-beta 1 mRNA. Evidence for a

A:Reference number: I46657; MUID:89054010; PMID:2461367  
A:Accession: I46657

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-390 <KON>

A:Cross-references: GB:M23703; NID:G755044; PIDN:AAA64616.1; PID:G755045  
C/Genetics:  
A:Gene: TGF-beta-1  
C:Superfamily: inhibin  
C:Keywords: growth factor

Query Match 100.0%; Score 96; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15  
|||||  
Db 318 HANFCLGCPYIWSL 332

## RESULT 8

transforming growth factor beta-1 - sheep  
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C/Date: 19-Dec-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
A:Accession: I46463; S45115  
R:Woodall, C.J.; McLaren, L.J.; Watt, N.J.  
Gene 150, 371-373, 1994

A>Title: Sequence and chromosomal localisation of the gene encoding ovine latent transfo  
A:Reference number: I46463; MUID:95121932; PMID:7821809

A:Accession: I46463  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA

A:Residues: 1-390 <WOO>  
A:Cross-references: UNIPROT:P50414; EMBL:X76916; NID:G496648; PIDN:CAA54242.1; PID:G49666  
A>Note: submitted to the EMBL Data Library, December 1993

C:Superfamily: inhibin

Query Match 100.0%; Score 96; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGCPYIWSL 15  
|||||  
Db 318 HANFCLGCPYIWSL 332

## RESULT 9

transforming growth factor beta-1 precursor - rat  
N/Alternate names: TGF type 2; TGF-beta

C/Species: Rattus norvegicus (Norway rat)  
C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
A:Accession: S10219; P70023; S02267  
R:Qian, S.W.; Kondatiah, P.; Roberts, A.B.; Sporn, M.B.

Nucleic Acids Res. 18, 3059, 1990  
A>Title: cDNA cloning by PCR of rat transforming growth factor beta-1.  
A:Reference number: S10219; MUID:90272425; PMID:2349108

A:Accession: S10219  
A:Molecule type: mRNA  
A:Residues: 1-390 <QIA>

A:Cross-references: UNIPROT:P17246; EMBL:X52498; NID:G57341; PIDN:CAA36741.1; PID:G57342  
R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.

J. Biochem. 106, 304-310, 1989  
A>Title: Purification and structural analysis of a latent form of transforming growth fa  
A:Reference number: P70023; MUID:90036779; PMID:2478527

A:Accession: P70023  
A:Molecule type: protein  
A:Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 <OKA>  
R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.

FEBS Lett. 242, 240-244, 1989

A/Title: One of two subunits of masking protein in latent TGF-beta is a part of pro-TGF-  
A/Reference number: S02267; MUID:89121078; PMID:2914605  
A/Accession: S02267  
A/Molecule type: protein  
A/Residues: 30-32,'X','34-38','Q','40-42','X','44 <OK2>  
C/Superfamily: Inhibin  
C/Keywords: glycoprotein; growth factor; integrin binding  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-278/Domain: propeptide #status experimental <PRO>  
F:244-246/Region: cell attachment (R-G-D) motif  
F:279-390/Product: transforming growth factor beta-1 #status predicted <MAT>  
F:82,136,176/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 96; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 8,3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYTWSL 15  
Db 318 HANFCLGPCPYTWSL 332

RESULT 10  
S01413  
transforming growth factor beta-1 precursor - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C/Accession: S01413  
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.  
Nucleic Acids Res. 16, 8730, 1988  
A/Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1).  
A/Reference number: S01413; MUID:88335639; PMID:3166520  
A/Accession: S01413  
A/Molecule type: DNA  
A/Residues: 1-391 <JAK>  
A/Cross-references: UNIPROT:P07200; EMBL:X12373; NID:963808; PIDN:CAA30933.1; PID:963805  
C/Superfamily: Inhibin  
C/Keywords: growth factor

Query Match 100.0%; Score 96; DB 2; Length 391;  
Best Local Similarity 100.0%; Pred. No. 8,3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYTWSL 15  
Db 319 HANFCLGPCPYTWSL 333

RESULT 11  
A41918  
transforming growth factor beta-4 precursor - chicken (fragment)  
N/Alternate names: TGF-beta 4  
C/Species: Gallus gallus (chicken)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C/Accession: A41918; A34941; S03110  
R:Burt, D.W.; Jakowlew, S.B.  
Mol. Endocrinol. 6, 989-992, 1992  
A/Title: Correction: a new interpretation of a chicken transforming growth factor-beta 4  
A/Reference number: A41918; MUID:92357039; PMID:1353860  
A/Accession: A41918  
A/Molecule type: mRNA  
A/Residues: 1-373 <BUR>  
A/Cross-references: UNIPROT:P09531; GB:M31160; GB:X08012; GB:S41706; NID:91262437; PIDN:  
A/Note: sequence extracted from NCBI backbone (NCBI:110186, NCBI:P:110187)  
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.  
Mol. Endocrinol. 2, 1186-1195, 1988  
A/Title: Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid end  
A/Reference number: A34941; MUID:89112198; PMID:2464131  
A/Accession: A34941  
A/Molecule type: mRNA  
A/Residues: 'MDPMISGPGSCGSPWPPGTAPWISGSRATASSCSTSSRVRAEVGGRAL',122-209,'D',211-373 <  
A/Cross-references: EMBL:X08012

A/Note: this sequence has been corrected in A41918  
C/Superfamily: Inhibin  
C/Keywords: glycoprotein; growth factor  
F:1/Domain: signal sequence (fragment) #status predicted <SIG>  
F:223-225/Region: cell attachment (R-G-D) motif  
F:260-373/Product: transforming growth factor beta-4 #status predicted <MAT>  
F:54,109,153/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 85.4%; Score 82; DB 2; Length 373;  
Best Local Similarity 92.3%; Pred. No. 9,3e-05;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ANFCLGPCPYTWS 14  
Db 302 ANFCLGPCPYTWS 314

RESULT 12  
A39489  
transforming growth factor beta-2 precursor - chicken  
N/Alternate names: TGF-beta2  
C/Species: Gallus gallus (chicken)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C/Accession: A39489; A61018; S25849  
R:Burt, D.W.; Paton, I.R.  
DNA Cell Biol. 10, 723-734, 1991  
A/Title: Molecular cloning and primary structure of the chicken transforming growth factor  
A/Reference number: A39489; MUID:92075163; PMID:1663775  
A/Accession: A39489  
A/Molecule type: DNA  
A/Residues: 1-412 <BUR>  
A/Cross-references: UNIPROT:P30371; GB:X58071; NID:963810; PIDN:CAA41101.1; PID:9833616;  
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.  
Growth Factors 2, 123-133, 1990  
A/Title: Complementary deoxyribonucleic acid cloning of an mRNA encoding transforming growth  
A/Reference number: A61018; MUID:90253805; PMID:2340183  
A/Accession: A61018  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-94,'G',96-244,'L',246-412 <JAK>  
C/Genetics: 115/1, 169/3, 214/1, 251/1, 309/2, 360/3  
A/Introns: 115/1, 169/3, 214/1, 251/1, 309/2, 360/3  
C/Keywords: growth factor; growth regulation; mitogen; transformation  
C/Superfamily: Inhibin  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-300/Domain: propeptide #status predicted <PRO>  
F:301-412/Product: transforming growth factor beta-2 #status predicted <MAT>

Query Match 80.2%; Score 77; DB 2; Length 412;  
Best Local Similarity 78.6%; Pred. No. 0.00055;  
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HANFCLGPCPYTWS 14  
Db 340 HANFCLGPCPYTWS 353

RESULT 13  
B61036  
transforming growth factor beta-5 precursor - African clawed frog  
C/Species: Xenopus laevis (African clawed frog)  
C/Date: 31-Dec-1993 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C/Accession: A34929; B61036  
R:Kondalath, P.; Sander, M.J.; Smith, J.M.; Fielde, A.; Roberts, A.B.; Sporn, M.B.; Melton, D.L.  
J. Biol. Chem. 265, 1089-1093, 1990  
A/Title: Identification of a novel transforming growth factor-beta (TGF-beta5) mRNA in X  
A/Reference number: A34929; MUID:90110090; PMID:2235601  
A/Accession: A34929  
A/Molecule type: mRNA  
A/Residues: 1-382 <KON>  
A/Cross-references: UNIPROT:P16176; GB:J05180; NID:9214821; PIDN:AAA49968.1; PID:9214822  
R:Roberts, A.B.; Rosa, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Rebbert, M.L.; Kondalath, P.  
Growth Factors 2, 135-147, 1990

A:Title: Isolation and characterization of TGF-beta2 and TGF-betas from medium condition  
A:Reference number: A61036; MUID:90253806; PMID:2340184  
A:Accession: B61036  
A:Molecule type: Protein  
A:Residues: 271-276,'X','278-284','XX',287-299 <ROB>  
C:Superfamily: Inhibin  
C:Keywords: growth factor  
F:271-382/Product: transforming growth factor beta-5 #status experimental <MAT>

Query Match 77.1%; Score 74; DB 2; Length 382;  
Best Local Similarity 78.6%; Pred. No. 0.0014;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ANFCLGCPYIWSL 15  
DB 311 ANFCLGNCPIYWSM 324

RESULT 14  
A61439  
transforming growth factor beta-2 - bovine  
N:Alternate names: cartilage-inducing factor B; MGF-a; milk growth factor a  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 07-Oct-1994 #sequence revision 07-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: A61439; A25485; B42320; S15389  
R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.  
J. Protein Chem. 10, 565-575, 1991  
A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta  
A:Reference number: A61439; MUID:92189724; PMID:1799413  
A:Accession: A61439  
A:Molecule type: Protein  
A:Residues: 1-112 <JIN>  
A:Cross-references: UNIPROT:P21214  
A:Experimental source: milk  
R:Seyedin, S.M.; Segarini, P.R.; Rosen, D.M.; Thompson, A.Y.; Bentz, H.; Graycar, J.  
J. Biol. Chem. 262, 1946-1949, 1987  
A:Title: Cartilage-inducing factor-B is a unique protein structurally and functionally  
A:Reference number: A25485; MUID:87137406; PMID:3469199  
A:Accession: A25485  
A:Molecule type: Protein  
A:Residues: 1-30 <SEX>  
A:Experimental source: Bone  
R:Ogawa, Y.; Schmidt, D.K.; Daesch, J.R.; Chang, R.J.; Glaeser, C.B.  
J. Biol. Chem. 267, 2325-2328, 1992  
A:Title: Purification and characterization of transforming growth factor-beta2.3 and -be  
A:Reference number: A42320; MUID:92129307; PMID:1733936  
A:Accession: B42320  
A:Molecule type: Protein  
A:Residues: 1-6,'X','8-14','XX',17-34 <OGA>  
A:Experimental source: bone  
R:Cox, D.A.; Buerk, R.R.  
Eur. J. Biochem. 197, 353-358, 1991  
A:Title: Isolation and characterization of milk growth factor, a transforming-growth-fac  
A:Reference number: S15389; MUID:91224126; PMID:2026157  
A:Accession: S15389  
A:Molecule type: Protein  
A:Residues: 1-16,'X','19 <COX>  
A:Experimental source: milk  
C:Superfamily: Inhibin  
C:Keywords: growth factor; growth regulation; heterodimer; homodimer

Query Match 72.9%; Score 70; DB 2; Length 112;  
Best Local Similarity 71.4%; Pred. No. 0.002;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWS 14  
DB 40 NAFCLGACPYIWS 53

RESULT 15  
WFXLB2  
transforming growth factor beta-2 precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)  
C:Date: 12-Feb-1993 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004  
C:Accession: S09510; A61036  
R:Rebberth, M.L.; Bhatia-Dey, N.; David, I.B.  
Nucleic Acids Res. 18, 2185, 1990  
A:Title: The sequence of TGF-beta2 from Xenopus laevis.  
A:Reference number: S09510; MUID:90245678; PMID:2336403  
A:Accession: S09510  
A:Molecule type: mRNA  
A:Residues: 1-413 <REB>  
A:Cross-references: UNIPROT:P17247; EMBL:X51817; NID:9414789; PIRN:CAA36116.1; PID:g6513  
R:Roberts, A.B.; Rosa, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Rebberth, M.L.; Kond  
Growth Factors 2, 135-147, 1990  
A:Title: Isolation and characterization of TGF-beta2 and TGF-betas from medium condition  
A:Reference number: A61036; MUID:90253806; PMID:2340184  
A:Accession: A61036  
A:Molecule type: Protein  
A:Residues: 302-307,'X','309-315','XX',318-319 <ROB>  
C:Superfamily: Inhibin  
C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-301/Domain: propeptide #status predicted <PRO>  
F:302-413/Product: transforming growth factor beta-2 #status predicted <MAT>  
F:72,140,241/Binding site: carboxyrate (Asn) (covalent) #status predicted

Query Match 72.9%; Score 70; DB 1; Length 413;  
Best Local Similarity 71.4%; Pred. No. 0.0059;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWS 14  
DB 341 NAFCLGACPYIWS 354

Search completed: June 14, 2005, 15:52:09  
Job time : 17.7308 secs



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: June 14, 2005, 15:51:20 ; Search time 78.4615 Seconds  
(without alignments)  
73.265 Million cell updates/sec

Title: US-09-831-253F-1

Perfect score: 96

Sequence: 1 HANFCLGCPYIWSL 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications\_AA:\*

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	96	100.0	51 9 US-09-864-761-47871	Sequence 47871, A
2	96	100.0	60 10 US-09-791-501-122	Sequence 122, App
3	96	100.0	70 16 US-10-812-642-122	Sequence 122, App
4	96	100.0	60 9 US-09-848-664-9	Sequence 9, Appl1
5	96	100.0	98 14 US-10-187-394-1	Sequence 14, Appl1
6	96	100.0	99 10 US-09-754-831A-48	Sequence 48, Appl1
7	96	100.0	99 17 US-10-671-317-48	Sequence 48, Appl1
8	96	100.0	112 9 US-09-813-271B-2	Sequence 2, Appl1
9	96	100.0	112 15 US-10-366-345-54	Sequence 54, Appl1
10	96	100.0	112 17 US-10-872-198-104	Sequence 104, App
11	96	100.0	113 9 US-09-813-398-13	Sequence 13, Appl1

12	96	100.0	113 16 US-10-826-324-13	Sequence 13, Appl1
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15	96 <td>100.0<td>114 13 US-10-115-406-21<th>Sequence 21, Appl1</th></td></td>	100.0 <td>114 13 US-10-115-406-21<th>Sequence 21, Appl1</th></td>	114 13 US-10-115-406-21 <th>Sequence 21, Appl1</th>	Sequence 21, Appl1
16	96 <td>100.0<td>114 13 US-10-154-333-23<th>Sequence 23, Appl1</th></td></td>	100.0 <td>114 13 US-10-154-333-23<th>Sequence 23, Appl1</th></td>	114 13 US-10-154-333-23 <th>Sequence 23, Appl1</th>	Sequence 23, Appl1
17	96 <td>100.0<td>114 16 US-10-704-223-21<th>Sequence 21, Appl1</th></td></td>	100.0 <td>114 16 US-10-704-223-21<th>Sequence 21, Appl1</th></td>	114 16 US-10-704-223-21 <th>Sequence 21, Appl1</th>	Sequence 21, Appl1
18	96 <td>100.0<td>115 9 US-09-859-211-47<th>Sequence 47, Appl1</th></td></td>	100.0 <td>115 9 US-09-859-211-47<th>Sequence 47, Appl1</th></td>	115 9 US-09-859-211-47 <th>Sequence 47, Appl1</th>	Sequence 47, Appl1
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36	96 <td>100.0<td>390 14 US-10-087-268-2<th>Sequence 2, Appl1</th></td></td>	100.0 <td>390 14 US-10-087-268-2<th>Sequence 2, Appl1</th></td>	390 14 US-10-087-268-2 <th>Sequence 2, Appl1</th>	Sequence 2, Appl1
37	96 <td>100.0<td>390 14 US-10-087-268-5<th>Sequence 5, Appl1</th></td></td>	100.0 <td>390 14 US-10-087-268-5<th>Sequence 5, Appl1</th></td>	390 14 US-10-087-268-5 <th>Sequence 5, Appl1</th>	Sequence 5, Appl1
38	96 <td>100.0<td>390 14 US-10-087-268-7<th>Sequence 7, Appl1</th></td></td>	100.0 <td>390 14 US-10-087-268-7<th>Sequence 7, Appl1</th></td>	390 14 US-10-087-268-7 <th>Sequence 7, Appl1</th>	Sequence 7, Appl1
39	96 <td>100.0<td>390 15 US-10-131-985-13<th>Sequence 13, Appl1</th></td></td>	100.0 <td>390 15 US-10-131-985-13<th>Sequence 13, Appl1</th></td>	390 15 US-10-131-985-13 <th>Sequence 13, Appl1</th>	Sequence 13, Appl1
40	96 <td>100.0<td>390 15 US-10-366-345-46<th>Sequence 46, Appl1</th></td></td>	100.0 <td>390 15 US-10-366-345-46<th>Sequence 46, Appl1</th></td>	390 15 US-10-366-345-46 <th>Sequence 46, Appl1</th>	Sequence 46, Appl1
41	96 <td>100.0<td>390 16 US-10-746-545-38<th>Sequence 38, Appl1</th></td></td>	100.0 <td>390 16 US-10-746-545-38<th>Sequence 38, Appl1</th></td>	390 16 US-10-746-545-38 <th>Sequence 38, Appl1</th>	Sequence 38, Appl1
42	96 <td>100.0<td>390 16 US-10-688-845-12<th>Sequence 12, Appl1</th></td></td>	100.0 <td>390 16 US-10-688-845-12<th>Sequence 12, Appl1</th></td>	390 16 US-10-688-845-12 <th>Sequence 12, Appl1</th>	Sequence 12, Appl1
43	96 <td>100.0<td>390 17 US-10-741-600-1307<th>Sequence 1307, Ap</th></td></td>	100.0 <td>390 17 US-10-741-600-1307<th>Sequence 1307, Ap</th></td>	390 17 US-10-741-600-1307 <th>Sequence 1307, Ap</th>	Sequence 1307, Ap
44	96 <td>100.0<td>390 17 US-10-741-600-1308<th>Sequence 1308, Ap</th></td></td>	100.0 <td>390 17 US-10-741-600-1308<th>Sequence 1308, Ap</th></td>	390 17 US-10-741-600-1308 <th>Sequence 1308, Ap</th>	Sequence 1308, Ap
45	96 <td>100.0<td>390 17 US-10-901-417-13<th>Sequence 13, Appl1</th></td></td>	100.0 <td>390 17 US-10-901-417-13<th>Sequence 13, Appl1</th></td>	390 17 US-10-901-417-13 <th>Sequence 13, Appl1</th>	Sequence 13, Appl1

#### ALIGNMENTS

RESULT 1

US-09-864-761-47871

/ Sequence 47871, Application US/09864761

/ Patent No. US20020048763A1

/ GENERAL INFORMATION:

/ APPLICANT: Penn, Sharon G.

/ APPLICANT: Rank, David R.

/ APPLICANT: Hanzel, David K.

/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

/ FILE REFERENCE: Aecmca-x-1

/ CURRENT APPLICATION NUMBER: US/09/864, 761

/ PRIOR FILING DATE: 2001-05-23

/ PRIOR APPLICATION NUMBER: US 60/180,312

/ PRIOR FILING DATE: 2000-02-04

/ PRIOR APPLICATION NUMBER: US 60/207,456

/ PRIOR FILING DATE: 2000-05-26

/ PRIOR APPLICATION NUMBER: US 09/632,366

/ PRIOR FILING DATE: 2000-08-03

/ PRIOR APPLICATION NUMBER: GB 24263, 6

/ PRIOR FILING DATE: 2000-10-04

/ PRIOR APPLICATION NUMBER: US 60/236,359

/ PRIOR FILING DATE: 2000-09-27

/ PRIOR APPLICATION NUMBER: PCT/US01/00666

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00667

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00664

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00669

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00665

/ PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47871
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011462.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.8
; OTHER INFORMATION: EST HUMAN HIT: BE737006.1, EVALUE 4.00e-28
; OTHER INFORMATION: SWISSPROT HIT: O19011, EVALUE 3.00e-29
US-09-864-761-47871
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Query Match          100.0%; Score 96; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. NO. 6.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 HANFCLGCPYIMSL 15
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Db      31 HANFCLGCPYIMSL 45
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RESULT 2
US-09-791-301-122
; Sequence 122, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
; APPLICANT: Pagratia, Nikos
; APPLICANT: Gold, Larry
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX 87/C
; CURRENT APPLICATION NUMBER: US/09/791,301
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
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; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-791-301-122
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Query Match          100.0%; Score 96; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. NO. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 HANFCLGCPYIMSL 15
         |||||
Db      40 HANFCLGCPYIMSL 54
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RESULT 3
US-10-812-642-122
; Sequence 122, Application US/10812642
; Publication No. US20040258656A1
; GENERAL INFORMATION:
; APPLICANT: Pagratia, Nikos
; APPLICANT: Gold, Larry
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/10/812,642
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/363,939A
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-812-642-122
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Query Match          100.0%; Score 96; DB 16; Length 60;
Best Local Similarity 100.0%; Pred. NO. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 HANFCLGCPYIMSL 15
         |||||
Db      40 HANFCLGCPYIMSL 54
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RESULT 4
US-09-848-664-9
; Sequence 9, Application US/09848664
; Patent No. US20020146414A1
; GENERAL INFORMATION:
; APPLICANT: Sakiyama-Elbert, Shelly E.
; APPLICANT: Hubbell, Jeffrey A.
```

TITLE OF INVENTION: Controlled Release of No. US2002014641A1-Heparin Binding Growth  
; TITLE OF INVENTION: Factors from Heparin Containing Matrices  
; FILE REFERENCE: ETH 108  
; CURRENT APPLICATION NUMBER: US/09/848,664  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: 09/298,084  
; PRIOR FILING DATE: 1999-04-22  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-848-664-9

Query Match 100.0%; Score 96; DB 9; Length 70;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGCPYIWSL 15  
Db 40 HANFCLGCPYIWSL 54

RESULT 5  
US-10-187-394-1  
; Sequence 1, Application US/10187394  
; Publication No. US2003017667A1  
; GENERAL INFORMATION:  
; APPLICANT: KECK, PETER  
; APPLICANT: SMART, JOHN  
; TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &  
; ADDRESS: THIBEAULT, LLP  
; STREET: 125 HIGH STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/187,394  
; FILING DATE: 28-JUNE-2002  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/496,398  
; FILING DATE: 02-FEB-2000  
; CLASSIFICATION:  
; APPLICATION NUMBER: US 08/478,097  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PITCHER ESQ. EDMUND R  
; REGISTRATION NUMBER: 27,829  
; REFERENCE/DOCKET NUMBER: STK-059CN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-248-7000  
; TELEFAX: 617-248-7100  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:

NAME/KEY: Protein  
; LOCATION: 1..98  
; OTHER INFORMATION: /note= "TGF-B1 SEQUENCE"  
US-10-187-394-1

Query Match 100.0%; Score 96; DB 14; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGCPYIWSL 15  
Db 26 HANFCLGCPYIWSL 40

RESULT 6  
US-09-754-831A-48  
; Sequence 48, Application US/09754831A  
; Publication No. US20030228345A1  
; GENERAL INFORMATION:  
; APPLICANT: Oppermann, Herman  
; APPLICANT: Kuberzampath, Thangavel  
; APPLICANT: Rueger, David  
; APPLICANT: Ozkaynak, Engin  
; TITLE OF INVENTION: Osteogenic Devices  
; FILE REFERENCE: STK-008CN  
; CURRENT APPLICATION NUMBER: US/09/754,831A  
; PRIOR FILING DATE: 2001-01-03  
; PRIOR APPLICATION NUMBER: US 08/375,901  
; PRIOR FILING DATE: 1995-01-20  
; PRIOR APPLICATION NUMBER: US 08/145,812  
; PRIOR FILING DATE: 1993-11-01  
; PRIOR APPLICATION NUMBER: US 07/995,345  
; PRIOR FILING DATE: 1992-12-22  
; PRIOR APPLICATION NUMBER: US 07/315,342  
; PRIOR FILING DATE: 1989-02-23  
; PRIOR APPLICATION NUMBER: US 07/232,630  
; PRIOR FILING DATE: 1988-08-15  
; PRIOR APPLICATION NUMBER: US 07/179,406  
; PRIOR FILING DATE: 1988-04-08  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 48  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TGF-beta-1  
US-09-754-831A-48

Query Match 100.0%; Score 96; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HANFCLGCPYIWSL 15  
Db 26 HANFCLGCPYIWSL 40

RESULT 7  
US-10-671-317-48  
; Sequence 48, Application US/10671317  
; Publication No. US20050054825A1  
; GENERAL INFORMATION:  
; APPLICANT: Oppermann, Herman  
; APPLICANT: Kuberzampath, Thangavel  
; APPLICANT: Rueger, David  
; APPLICANT: Ozkaynak, Engin  
; TITLE OF INVENTION: Osteogenic Devices  
; FILE REFERENCE: STK-010C3  
; CURRENT APPLICATION NUMBER: US/10/671,317  
; PRIOR FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: US 09/956,582  
; PRIOR FILING DATE: 2001-09-19

PRIOR APPLICATION NUMBER: US 09/074,299  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: US 08/417,071  
PRIOR FILING DATE: 1995-04-04  
PRIOR APPLICATION NUMBER: US 08/145,812  
PRIOR FILING DATE: 1993-11-01  
PRIOR APPLICATION NUMBER: US 07/995,345  
PRIOR FILING DATE: 1989-12-22  
PRIOR APPLICATION NUMBER: US 07/315,342  
PRIOR FILING DATE: 1989-02-23  
PRIOR APPLICATION NUMBER: US 07/232,630  
PRIOR FILING DATE: 1988-08-15  
PRIOR APPLICATION NUMBER: US 07/179,406  
PRIOR FILING DATE: 1988-04-08  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 48  
LENGTH: 99  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: TGF-beta-1  
US-10-671-317-48

Query Match 100.0%; Score 96; DB 17; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGPCPYIWSL 15  
Db 26 HANFCLGPCPYIWSL 40

## RESULT 8

US-09-813-271B-2  
Sequence 2, Application US/09813271B  
Patent No. US20020115834A1  
GENERAL INFORMATION:

APPLICANT:

(A) Nico Carletti  
TITLE OF INVENTION: New process for the production of  
biologically active protein

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. US20020115834A1artis Patent Department  
STREET: 564 Morris Avenue  
City: Summit

STATE: New Jersey

COUNTRY: USA

ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/813,271B

FILING DATE: 20-Mar-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/02719

FILING DATE: 12-Jul-95

APPLICATION NUMBER: EPO 94810439.3

FILING DATE: 25-Jul-94

ATTORNEY/AGENT INFORMATION:

NAME: Pfeiffer, Henna J.

REGISTRATION NUMBER: 22640

REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN

TELEPHONE: (908) 522-6940

TELEFAX: (908) 522-6955

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-813-271B-2

Query Match 100.0%; Score 96; DB 9; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGPCPYIWSL 15  
Db 40 HANFCLGPCPYIWSL 54

## RESULT 9

US-10-366-345-54  
Sequence 54, Application US/10366345  
Publication No. US20030224501A1  
GENERAL INFORMATION:

APPLICANT: Young, et al.

TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and

FILE REFERENCE: P1189

CURRENT APPLICATION NUMBER: US/10/366,345

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.2

SEQ ID NO 54

LENGTH: 112

TYPE: PRT

ORGANISM: Homo sapiens

US-10-366-345-54

Query Match 100.0%; Score 96; DB 15; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HANFCLGPCPYIWSL 15  
Db 40 HANFCLGPCPYIWSL 54

## RESULT 10

US-10-872-198-104  
Sequence 104, Application US/10872198  
Publication No. US20050002897A1  
GENERAL INFORMATION:

APPLICANT: Ulrich HAUTPS

APPLICANT: Andre KOLTERMAN

APPLICANT: Andreas SCHEIDIG

APPLICANT: Christian VOETSMER

APPLICANT: Ulrich Kettling

TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF

FILE REFERENCE: 04156.000204

CURRENT APPLICATION NUMBER: US/10/872,198

CURRENT FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 60/543,518

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/524,960

PRIOR FILING DATE: 2003-11-25

PRIOR APPLICATION NUMBER: EP 04003058

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: EP 03025871

PRIOR FILING DATE: 2003-11-11

PRIOR APPLICATION NUMBER: EP 03025851

PRIOR FILING DATE: 2003-11-10

PRIOR APPLICATION NUMBER: EP 03013819

PRIOR FILING DATE: 2003-06-18

NUMBER OF SEQ ID NOS: 149

SOFTWARE: PatentIn version 3.1

SEQ ID NO 104

LENGTH: 112



TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-872-198-104

Query Match 100.0%; Score 96; DB 17; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15  
DB 40 HANFCLGCPYIWSL 54

RESULT 11  
US-09-813-398-13  
Sequence 13, Application US/09813398  
Patent No. US20020169292A1  
GENERAL INFORMATION:  
APPLICANT: Mariusz W. Szkudlinski  
APPLICANT: Bruce D. Weintraub  
APPLICANT: University of Maryland  
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS  
FILE REFERENCE: USFMD.003C1  
CURRENT FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: PCT/US99/05908  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: PCT/US98/19772  
PRIOR FILING DATE: 1998-09-22  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 113  
TYPE: PRT  
ORGANISM: HOMO SAPIEN  
US-09-813-398-13

Query Match 100.0%; Score 96; DB 9; Length 113;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15  
DB 41 HANFCLGCPYIWSL 55

RESULT 12  
US-10-826-324-13  
Sequence 13, Application US/10826324  
Publication No. US20040265972A1  
GENERAL INFORMATION:  
APPLICANT: Bruce D. Weintraub  
APPLICANT: Mariusz W. Szkudlinski  
APPLICANT: University of Maryland  
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS  
FILE REFERENCE: USFMD.003C1  
CURRENT APPLICATION NUMBER: US/10/826,324  
CURRENT FILING DATE: 2004-04-19  
PRIOR APPLICATION NUMBER: US/09/813,398  
PRIOR FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: PCT/US99/05908  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: PCT/US98/19772  
PRIOR FILING DATE: 1998-09-22  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 113  
TYPE: PRT  
ORGANISM: HOMO SAPIEN  
US-10-826-324-13

Query Match 100.0%; Score 96; DB 16; Length 113;

Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15  
DB 41 HANFCLGCPYIWSL 55

RESULT 13  
US-09-389-705-23  
Sequence 23, Application US/09389705  
Publication No. US20010018509A1  
GENERAL INFORMATION:  
APPLICANT: JOHNS HOPKINS UNIVERSITY  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ  
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/389,705  
FILING DATE: 03-Sep-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/153,733  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: WETHERELL, JR. Ph.D., JOHN R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: FD2279 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta 1  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..114  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-389-705-23

Query Match 100.0%; Score 96; DB 9; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFCLGCPYIWSL 15  
DB 42 HANFCLGCPYIWSL 56

RESULT 14  
US-09-813-459-22  
Sequence 22, Application US/09813459  
Patent No. US20020107369A1  
GENERAL INFORMATION:  
APPLICANT: Lee, Se-jin  
Cunningham, No. US20020107369A1

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Judas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/813,459  
FILING DATE: 20-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/624,635  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D., John R.,  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-3054  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-1  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..114  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-813-459-22  
Query Match 100.0%; Score 96; DB 9; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HANFLGPGPYIWSL 15  
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Db 42 HANFLGPGPYIWSL 56  
RESULT 15  
US-10-115-406-21  
Sequence 21, Application US/10115406  
Publication No. US20020127612A1  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
APPLICANT: LEE, Se-Jin  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9  
FILE REFERENCE: JHU1190-3  
CURRENT APPLICATION NUMBER: US/10/115,406  
CURRENT FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: 09/301,520  
PRIOR FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: US 09/172,062  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: US 08/491,835  
PRIOR FILING DATE: 1995-10-23  
PRIOR APPLICATION NUMBER: PCT/US94/00685  
PRIOR FILING DATE: 1994-01-12  
PRIOR APPLICATION NUMBER: US 08/003,303  
PRIOR FILING DATE: 1993-01-12

NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 21  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-115-406-21

Query Match 100.0%; Score 96; DB 13; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HANFLGPGPYIWSL 15  
|||  
Db 42 HANFLGPGPYIWSL 56

Search completed: June 14, 2005, 16:14:52  
Job time : 79.4615 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model.

Run on: November 14, 2004, 12:54:46 ; Search time 136 Seconds  
(without alignments)  
31.219 Million cell updates/sec

Title: US-09-831-253F-3  
Perfect score: 63  
Sequence: 1 TSLDATM1WTM 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 1568699 seqs, 35381937 residues  
Total number of hits satisfying chosen parameters: 199616

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	29	46.0	7	9	US-09-758-128-44 Sequence 41, Appl
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5	29	46.0	7	9	US-09-758-128-41 Sequence 41, Appl
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7	29	46.0	7	9	US-09-758-128-41 Sequence 41, Appl
8	29	46.0	7	10	US-09-861-661-41 Sequence 44, Appl
9	29	46.0	7	10	US-09-861-661-44 Sequence 44, Appl
10	27	42.9	10	14	US-10-062-109A-642 Sequence 642, App
11	26	41.3	9	15	US-10-005-480A-642 Sequence 642, App
12	25	39.7	8	14	US-10-182-252A-685 Sequence 685, App
13	25	39.7	9	14	US-10-190-082-602 Sequence 602, App
					US-10-357-935-20 Sequence 20, Appl

14	25	39.7	9	15	US-10-182-252A-632 Sequence 632, App
15	25	39.7	9	15	US-10-182-252A-657 Sequence 657, App
16	25	39.7	9	15	US-10-182-252A-1216 Sequence 1216, Ap
17	25	39.7	10	14	US-10-200-708-79 Sequence 79, Appl
18	25	39.7	10	14	US-10-200-708-501 Sequence 501, Appl
19	25	39.7	11	10	US-09-755-109-7 Sequence 7, Appl
20	25	39.7	12	9	US-09-823-823-44 Sequence 44, Appl
21	25	39.7	12	9	US-09-840-277-69 Sequence 69, Appl
22	25	39.7	12	9	US-09-823-823-44 Sequence 44, Appl
23	25	39.7	12	9	US-10-609-217-151 Sequence 151, App
24	25	39.7	12	15	US-10-632-388-151 Sequence 151, App
25	25	39.7	12	15	US-10-651-723-151 Sequence 151, App
26	25	39.7	12	15	US-10-645-761-151 Sequence 151, App
27	25	39.7	12	15	US-10-666-696-151 Sequence 151, App
28	25	39.7	12	15	US-10-653-048-151 Sequence 151, App
29	24	38.1	7	15	US-10-651-165-170 Sequence 170, App
30	24	38.1	9	10	US-09-997-209-82 Sequence 82, Appl
31	24	38.1	9	15	US-10-182-252A-3 Sequence 3, Appl
32	24	38.1	9	15	US-10-182-252A-215 Sequence 215, Appl
33	24	38.1	9	15	US-10-182-252A-617 Sequence 617, App
34	24	38.1	9	15	US-10-182-252A-631 Sequence 631, App
35	24	38.1	9	15	US-10-182-252A-656 Sequence 656, App
36	24	38.1	9	15	US-10-182-252A-658 Sequence 658, App
37	24	38.1	11	10	US-10-431-206-82 Sequence 82, Appl
38	24	38.1	11	10	US-09-809-391-551 Sequence 551, App
39	24	38.1	11	10	US-09-882-171-551 Sequence 551, App
40	24	38.1	11	14	US-10-092-908-58 Sequence 58, Appl
41	24	38.1	11	14	US-10-164-861-551 Sequence 551, App
42	23	36.5	9	10	US-09-845-042-27 Sequence 27, Appl
43	23	36.5	9	14	US-10-062-109A-13 Sequence 13, Appl
44	23	36.5	9	14	US-10-005-480A-13 Sequence 13, Appl
45	23	36.5	9	15	US-10-182-252A-630 Sequence 630, Appl

## ALIGNMENTS

RESULT 1  
US-09-758-128-41  
Sequence 41, Application US/09758128  
Patent No. US20020107187A1  
GENERAL INFORMATION:  
APPLICANT: KINGSTON, David J.  
APPLICANT: GERRARY, No. US20020107187A1man L.  
INVENTOR: WESTBROOK, Simon L.  
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
FILE REFERENCE: 016766/0214  
CURRENT APPLICATION NUMBER: US/09/758,128  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 09/194,218  
PRIOR FILING DATE: 1999-02-05  
PRIOR APPLICATION NUMBER: AU P19990  
PRIOR FILING DATE: 1996-05-22  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 41  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-758-128-41  
Query Match  
Best Local Similarity 46.0%; Score 29; DB 9; Length 7;  
Matches 6; Conservative 1; Mismatches 0; Indels 0;  
DB 1 TSLDATV 7  
RESULT 2  
US-09-758-128-44

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73.285 Million cell updates/sec

Title: US-09-831-253F-2  
Perfect score: 89  
Sequence: 1 FCLGPCPYIWSLDT 14

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1710399

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 18: /cgn2\_6/ptodata/2/pubpaa/US10F\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	89	100.0	60	10	US-09-791-301-122
3	89	100.0	60	16	US-10-812-642-122
4	89	100.0	70	9	US-09-848-664-9
5	89	100.0	98	14	US-10-187-394-1
6	89	100.0	112	9	US-09-813-271B-2
7	89	100.0	112	15	US-10-366-345-54
8	89	100.0	112	17	US-10-872-198-104
9	89	100.0	113	9	US-09-813-398-13
10	89	100.0	113	16	US-10-826-324-13
11	89	100.0	114	9	US-09-389-705-23

12	89	100.0	114	9	US-09-813-459-22
13	89	100.0	114	13	US-10-115-406-21
14	89	100.0	114	14	US-10-154-333-23
15	89	100.0	114	16	US-10-704-223-21
16	89	100.0	115	9	US-09-859-211-47
17	89	100.0	115	9	US-09-880-708-25
18	89	100.0	115	10	US-09-872-856-47
19	89	100.0	115	14	US-10-335-483-29
20	89	100.0	115	15	US-10-463-973-47
21	89	100.0	115	15	US-10-693-536-19
22	89	100.0	115	16	US-10-758-210-19
23	89	100.0	139	13	US-10-002-278-8
24	89	100.0	185	16	US-10-781-866-52
25	89	100.0	218	16	US-10-781-866-51
26	89	100.0	315	10	US-09-214-592-25
27	89	100.0	390	9	US-09-756-283A-23
28	89	100.0	390	10	US-09-214-592-20
29	89	100.0	390	10	US-09-214-592-23
30	89	100.0	390	10	US-09-214-592-26
31	89	100.0	390	10	US-09-214-592-28
32	89	100.0	390	10	US-09-214-592-29
33	89	100.0	390	10	US-09-214-592-33
34	89	100.0	390	14	US-10-087-268-2
35	89	100.0	390	14	US-10-087-268-5
36	89	100.0	390	14	US-10-087-268-1
37	89	100.0	390	14	US-10-131-885-13
38	89	100.0	390	15	US-10-366-345-46
39	89	100.0	390	16	US-10-746-845-38
40	89	100.0	390	16	US-10-688-845-12
41	89	100.0	390	17	US-10-741-600-1307
42	89	100.0	390	17	US-10-741-600-1308
43	89	100.0	390	17	US-10-901-417-13
44	89	100.0	391	10	US-09-214-592-17
45	89	100.0	391	17	US-10-741-600-1309

## ALIGNMENTS

RESULT 1  
US-09-864-761-47871  
Sequence 47871, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecm:ica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263, 6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 47871  
LENGTH: 51  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC011462.3  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.8  
OTHER INFORMATION: EST HUMAN HIT: BE737006.1, EVALUE 4.00e-28  
OTHER INFORMATION: SWISSPROT HIT: O19011, EVALUE 3.00e-29  
US-09-864-761-47871

Query Match 100.0%; Score 89; DB 9; Length 51;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGPCPYIWSLDT 14  
Db 34 FCLGPCPYIWSLDT 47

RESULT 2  
US-09-791-301-122  
Sequence 122, Application US/09791301  
Publication No. US20030064943A1  
GENERAL INFORMATION:  
APPLICANT: Pagratzis, Nikos  
APPLICANT: Lochrie, Michael  
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
FILE REFERENCE: NEX 87/C  
CURRENT APPLICATION NUMBER: US/09/791,301  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/046,247  
PRIOR FILING DATE: 1998-03-23  
PRIOR APPLICATION NUMBER: 08/458,424  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: 07/714,131  
PRIOR FILING DATE: 1991-06-10  
PRIOR APPLICATION NUMBER: 07/931,473  
PRIOR FILING DATE: 1992-08-17  
PRIOR APPLICATION NUMBER: 07/964,624  
PRIOR FILING DATE: 1992-10-21  
PRIOR APPLICATION NUMBER: 08/117,991  
PRIOR FILING DATE: 1993-09-08  
PRIOR APPLICATION NUMBER: 07/536,428  
PRIOR FILING DATE: 1990-06-11  
PRIOR APPLICATION NUMBER: 09/363,939  
PRIOR FILING DATE: 1999-07-25  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 122

LENGTH: 60  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-791-301-122

Query Match 100.0%; Score 89; DB 10; Length 60;  
Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGPCPYIWSLDT 14  
Db 43 FCLGPCPYIWSLDT 56

RESULT 3  
US-10-812-642-122  
Sequence 122, Application US/10812642  
Publication No. US20040258656A1  
GENERAL INFORMATION:  
APPLICANT: Pagratzis, Nikos  
APPLICANT: Lochrie, Michael  
TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and  
FILE REFERENCE: NEX87  
CURRENT APPLICATION NUMBER: US/10/812,642  
PRIOR FILING DATE: 2004-03-30  
PRIOR APPLICATION NUMBER: US/09/363,939A  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: 09/046,247  
PRIOR FILING DATE: 1998-03-23  
PRIOR APPLICATION NUMBER: 08/458,424  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: 07/714,131  
PRIOR FILING DATE: 1991-06-10  
PRIOR APPLICATION NUMBER: 07/931,473  
PRIOR FILING DATE: 1992-08-17  
PRIOR APPLICATION NUMBER: 07/964,624  
PRIOR FILING DATE: 1992-10-21  
PRIOR APPLICATION NUMBER: 08/117,991  
PRIOR FILING DATE: 1993-09-08  
PRIOR APPLICATION NUMBER: 07/536,428  
PRIOR FILING DATE: 1990-06-11  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 122  
LENGTH: 60  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-812-642-122

Query Match 100.0%; Score 89; DB 16; Length 60;  
Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGPCPYIWSLDT 14  
Db 43 FCLGPCPYIWSLDT 56

RESULT 4  
US-09-848-664-9  
Sequence 9, Application US/09848664  
Patent No. US20020146414A1  
GENERAL INFORMATION:  
APPLICANT: Sakiyama-Elbert, Shelly E.  
APPLICANT: Hubbard, Jeffrey A.

;; TITLE OF INVENTION: Controlled Release of No. US2002014641A1-Heparin Binding Growth  
;; FILE OF INVENTION: Factors from Heparin Containing Matrices  
;; FILE REFERENCE: ETH 108  
;; CURRENT APPLICATION NUMBER: US/09/848,664  
;; PRIOR FILING DATE: 2001-05-03  
;; PRIOR APPLICATION NUMBER: 09/298,084  
;; NUMBER OF SEQ ID NOS: 31  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO: 9  
;; LENGTH: 70  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-848-664-9

Query Match 100.0%; Score 89; DB 9; Length 70;  
Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14  
|||  
Db 43 FCLGPCPYIWSLDT 56

RESULT 5  
US-10-187-394-1  
; Sequence 1, Application US/10187394  
; Publication No. US20030176667A1  
; GENERAL INFORMATION:  
; APPLICANT: KECK, PETER  
; APPLICANT: SMART, JOHN  
; TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &  
; ADDRESS: THIBEAULT, LLP  
; STREET: 125 HIGH STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/187,394  
; FILING DATE: 28-JUNE-2002  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/496,398  
; FILING DATE: 02-FEB-2000  
; CLASSIFICATION:  
; APPLICATION NUMBER: US 08/478,097  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PITCHER ESQ, EDMUND R  
; REGISTRATION NUMBER: 27,829  
; REFERENCE/DOCKET NUMBER: STR-059CN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-248-7000  
; TELEFAX: 617-248-7100  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:

;; NAME/KEY: Protein  
;; LOCATION: 1..98  
;; OTHER INFORMATION: /note="TGF-B1 SEQUENCE"  
US-10-187-394-1

Query Match 100.0%; Score 89; DB 14; Length 98;  
Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14  
|||  
Db 29 FCLGPCPYIWSLDT 42

RESULT 6  
US-09-813-271B-2  
; Sequence 2, Application US/09813271B  
; Patent No. US20020115834A1  
; GENERAL INFORMATION:  
; APPLICANT: (A) Nisco Cerletti  
; TITLE OF INVENTION: New process for the production of  
; biologically active protein  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. US20020115834A1artis Patent Department  
; STREET: 564 Morris Avenue  
; CITY: Summit  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07901  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/813,271B  
; FILING DATE: 20-Mar-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/02719  
; FILING DATE: 12-Jul-95  
; APPLICATION NUMBER: EPO 94810439.3  
; FILING DATE: 25-Jul-94  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pfeiffer, Henna J.  
; REGISTRATION NUMBER: 22640  
; REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 522-6940  
; TELEFAX: (908) 522-6955  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-813-271B-2

Query Match 100.0%; Score 89; DB 9; Length 112;  
Best Local Similarity 100.0%; Pred. No. 6.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14  
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Db 43 FCLGPCPYIWSLDT 56

RESULT 7  
US-10-366-345-54  
; Sequence 54, Application US/10366345  
; Publication No. US2003024501A1

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? GENERAL INFORMATION:
? APPLICANT: Young, et al.
? TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and
? TITLE OF INVENTION: Antibodies
? FILE REFERENCE: P1189
? CURRENT APPLICATION NUMBER: US/10/366,345
? CURRENT FILING DATE: 2003-02-14
? NUMBER OF SEQ ID NOS: 77
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 54
? LENGTH: 112
? TYPE: PRT
? ORGANISM: Homo sapiens
? OS-10-366-345-54

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Query Match	100.0%	Score 89;	DB 15;	Length 112;
Best Local Similarity	100.0%	Pred. No.	6.5e-05;	
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 FCLGPCPYIWSLDT 14
        |||||
Db      43 FCLGPCPYIWSLDT 56
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RESULT 8  
US-10-872-198-104  
; Sequence 104, Application US/10872198  
; Publication No. US20050002897A1

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APPLICANT: Andre KOLTERMANN
APPLICANT: Andreas SCHEIDIG
APPLICANT: Christian VOETSMETER
APPLICANT: Ulrich Ketting
TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
FILE REFERENCE: 04156.000204
CURRENT APPLICATION NUMBER: US/10/872,198
CURRENT FILING DATE: 2004-06-18
PRIORITY APPLICATION NUMBER: 60/545,518
PRIORITY FILING DATE: 2004-02-11
PRIORITY APPLICATION NUMBER: 60/524,960
PRIORITY FILING DATE: 2003-11-25
PRIORITY APPLICATION NUMBER: EP 04003058
PRIORITY FILING DATE: 2004-02-11
PRIORITY APPLICATION NUMBER: EP 03025871
PRIORITY FILING DATE: 2003-11-11
PRIORITY APPLICATION NUMBER: EP 03025851
PRIORITY FILING DATE: 2003-11-10
PRIORITY APPLICATION NUMBER: EP 03013819
PRIORITY FILING DATE: 2003-06-18
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 104
LENGTH: 112
TYPE: PRT
ORGANISM: Homo sapiens
US-10-872-198-104

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Query Match	100.0%	Score 89;	DB 17;	length 112;
Best Local Similarity	100.0%	Pred. NC	6.5e-05;	
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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QY      1 FCLGPCPYIWSLDT 14
          |||||
Db      43 FCLGPCPYIWSLDT 56
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RESULT 9  
US-09-813-398-13  
; Sequence 13, Application US/09813398  
; Patent No. US20020169282A1  
; GENERAL INFORMATION:  
; APPLICANT: Bruce D. Weintraub

```

1  APPLICANT: Maritsz W. Szudliniak
2  APPLICANT: University of Maryland
3  TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
4  FILE REFERENCE: US/09/813,398
5  CURRENT APPLICATION NUMBER: US/09/813,398
6  PRIOR FILING DATE: 2001-03-20
7  PRIOR APPLICATION NUMBER: PCT/US99/05908
8  PRIOR FILING DATE: 1999-03-19
9  PRIOR APPLICATION NUMBER: PCT/US99/19772
10 PRIOR FILING DATE: 1998-09-22
11 NUMBER OF SEQ. ID NOS: 41
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 13
14 LENGTH: 113
15 TYPE: PRT
16 ORGANISM: HOMO SAPIEN
17 US-09-813-398-13

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Query Match	100.0%;	Score 89;	DB 9;	Length 113;
Best Local Similarity	100.0%;	Pred. No. 6.5e-05;		
Matches 14; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 FCLGPCPYIWSLDT 14
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Db      44 FCLGPCPYIWSLDT 57
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RESULT 10
US-10-826-324-13
? Sequence 13, Application US/10826324
? Publication No. US20040265972A1
? GENERAL INFORMATION:
? APPLICANT: Bruce D. Weistrub
? APPLICANT: Mariusz W. Szchulnski
? APPLICANT: University of Maryland
? TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
? FILE REFERENCE: US/06M,003C1
? CURRENT APPLICATION NUMBER: US/10/826,324
? CURRENT FILING DATE: 2004-04-19
? PRIOR APPLICATION NUMBER: US/09/813,398
? PRIOR FILING DATE: 2001-03-20
? PRIOR APPLICATION NUMBER: PCT/US99/05908
? PRIOR FILING DATE: 1999-03-19
? PRIOR APPLICATION NUMBER: PCT/US98/19772
? PRIOR FILING DATE: 1998-09-22
? NUMBER OF SEQ ID NOS: 41
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 13
? LENGTH: 113
? TYPE: PRT
? ORGANISM: HOMO SAPIEN
? US-10-826-324-13

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Query Match	100.0%;	Score 89;	DB 16;	Length 113;
Best Local Similarity	100.0%;	Pred. No. 6.5e-05;		
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	FCLG	PCPY	IWSL	DT	14
Db	44	FCLG <td>PCPY <td>IWSL <td>DT</td> <td>57</td> </td></td>	PCPY <td>IWSL <td>DT</td> <td>57</td> </td>	IWSL <td>DT</td> <td>57</td>	DT	57

RESULT 11  
US-09-389-705-23  
; Sequence 23, Application US/09389705  
; Publication No. US20010018509A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHNS HOPKINS UNIVERSITY  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ  
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
;



CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/389,705  
FILING DATE: 03-Sep-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/153,733  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: WETHERELL, JR. Ph.D., JOHN R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD2279 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta 1  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..114  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-389-705-23  
Query Match 100.0%; Score 89; DB 9; Length 114;  
Best Local Similarity 100.0%; Pred. No. 6.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FCLGCPYIWSLDT 14  
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Db 45 FCLGCPYIWSLDT 58  
RESULT 12  
US-09-813-459-22  
Sequence 22, Application US/09813459  
Patent No. US20020107369A1  
GENERAL INFORMATION:  
APPLICANT: Lee, Se-jin  
Cunningham, No. US20020107369A1  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESS: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/813,459  
FILING DATE: 20-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/624,635  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D., John R.,  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-3054  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-1  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..114  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-813-459-22  
Query Match 100.0%; Score 89; DB 9; Length 114;  
Best Local Similarity 100.0%; Pred. No. 6.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FCLGCPYIWSLDT 14  
|||  
Db 45 FCLGCPYIWSLDT 58  
RESULT 13  
US-10-115-406-21  
Sequence 21, Application US/10115406  
Publication No. US20020127612A1  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
APPLICANT: Lee, Se-jin  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9  
FILE REFERENCE: JH01190-3  
CURRENT APPLICATION NUMBER: US/10/115,406  
PRIOR FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: 09/301,520  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: US 09/172,062  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: US 08/491,835  
PRIOR FILING DATE: 1995-10-23  
PRIOR APPLICATION NUMBER: PCT/US94/00685  
PRIOR FILING DATE: 1994-01-12  
PRIOR APPLICATION NUMBER: US 08/003,303  
PRIOR FILING DATE: 1993-01-12  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 21  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-115-406-21  
Query Match 100.0%; Score 89; DB 13; Length 114;  
Best Local Similarity 100.0%; Pred. No. 6.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FCLGCPYIWSLDT 14  
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Db 45 FCLGCPYIWSLDT 58  
RESULT 14  
US-10-154-333-23

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; Sequence 23, Application US/10154333
; Publication No. US20030109684A1
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/154,333
; FILING DATE: 21-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/389,705
; FILING DATE: 03-Sep-1999
; APPLICATION NUMBER: 09/153,733
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph. D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta 1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-154-333-23

Query Match 100.0%; Score 89; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14
   |||||
DB 45 FCLGPCPYIWSLDT 58

RESULT 15
US-10-704-223-21
; Sequence 21, Application US/10704223
; Publication No. US20040152143A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; APPLICANT: LEE, Se-jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; FILE REFERENCE: JH01190-7
; CURRENT APPLICATION NUMBER: US/10/704,223
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 10/115,406
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US 09/301,520
; PRIOR FILING DATE: 1999-04-28
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; PRIOR APPLICATION NUMBER: US 09/172,062
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/491,835
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: PCT/US94/00665
; PRIOR FILING DATE: 1994-01-12
; PRIOR APPLICATION NUMBER: US 08/003,303
; PRIOR FILING DATE: 1993-01-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-704-223-21

Query Match 100.0%; Score 89; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIWSLDT 14
   |||||
DB 45 FCLGPCPYIWSLDT 58
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Search completed: June 14, 2005, 16:14:52  
Job time : 73.2308 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:29:15 ; Search time 80.2308 Seconds  
(without alignments)  
67.488 Million cell updates/sec

Title: US-09-831-253F-2  
Perfect score: 89  
Sequence: 1 FCLGCPYIWSLDT 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	89	100.0	14	AAV92946	AAV92946 Transform
3	89	100.0	21	AAV92982	AAV92982 Transform
4	89	100.0	23	AAV92983	AAV92983 Transform
5	89	100.0	23	AAV92954	AAV92954 Transform
6	89	100.0	25	ABU08659	ABU08659 Human tra
7	89	100.0	25	ABU79533	ABU79533 Human tra
8	89	100.0	50	AAV90828	AAV90828 Pre-trans
9	89	100.0	51	AAV90475	AAV90475 Sequence
10	89	100.0	51	AAV78788	AAV78788 Human tra
11	89	100.0	51	ABW43879	ABW43879 Peptide #
12	89	100.0	51	AAV37799	AAV37799 Peptide #
13	89	100.0	51	AAV77605	AAV77605 Human bon
14	89	100.0	51	ABG46640	ABG46640 Human pep
15	89	100.0	60	AAW68685	AAW68685 Human TGF
16	89	100.0	62	AAW30331	AAW30331 Fragment
17	89	100.0	65	AAV22135	AAV22135 PDGI subu
18	89	100.0	98	AAV11942	AAV11942 Truncated
19	89	100.0	98	AAV16697	AAV16697 MO914235
20	89	100.0	98	AAV92554	AAV92554 TGF-beta
21	89	100.0	98	AAV09519	AAV09519 Human TGF
22	89	100.0	98	AAW02785	AAW02785 Human TGF
23	89	100.0	112	AAW08142	AAW08142 Platelet-
24	89	100.0	112	AAW04076	AAW04076 Sequence
25	89	100.0	112	AAV12402	AAV12402 Transform

26	89	100.0	112	2	AAV22134	AAV22134 PDGI subu
27	89	100.0	112	2	AAV43263	AAV43263 TGF-beta
28	89	100.0	112	2	AAV39643	AAV39643 Transform
29	89	100.0	112	2	AAV39645	AAV39645 Transform
30	89	100.0	112	2	AAV42311	AAV42311 Recombina
31	89	100.0	112	2	AAV92773	AAV92773 Human TGF
32	89	100.0	112	2	AAV91956	AAV91956 Human tra
33	89	100.0	112	2	AAV08173	AAV08173 TGF-beta
34	89	100.0	112	2	AAV78781	AAV78781 Human tra
35	89	100.0	112	2	AAV97091	AAV97091 The matur
36	89	100.0	112	2	AAV08299	AAV08299 Human gro
37	89	100.0	112	2	AAW84207	AAW84207 Transform
38	89	100.0	112	3	AAV67950	AAV67950 Human tra
39	89	100.0	112	3	AAV92010	AAV92010 Human tra
40	89	100.0	112	4	AAV35937	AAV35937 TGF-beta
41	89	100.0	112	5	AAV51939	AAV51939 Human TGF
42	89	100.0	112	6	ABU08656	ABU08656 Human tra
43	89	100.0	112	8	ADH11598	ADH11598 Human bon
44	89	100.0	112	8	ABW79530	ABW79530 Human tra
45	89	100.0	114	2	AAV39638	AAV39638 Human tra

## ALIGNMENTS

RESULT 1  
AAV92966 standard; peptide, 14 AA.

AAV92966;

08-NOV-2000 (first entry)

Transforming growth factor inhibitory peptide P12.

Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; minotape; cirrhosis.

Homo sapiens.

WO200031135-A1.

02-JUN-2000.

23-NOV-1999; 99WO-ES000375.

24-NOV-1998; 98ES-00002465.

(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

Ezquerro Saenz IJ, Laarte Sagatibelza JJ, Prieto Valtuena J;

Borras Cuesta F;

WPI, 2000-411935/35.

Peptides that antagonize binding of transforming growth factor beta1, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.

Disclosure; Page 22; 86pp; Spanish.

The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-beta1 and/or its receptors. Peptides AAV92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-beta1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis.

### RESULT 3

[illegible]

OS Homo sapiens.  
XX  
XX W0200031135-A1.  
XX  
XX 02-JUN-2000.  
XX  
XX 23-NOV-1999; 99WO-ES000375.  
XX  
XX 24-NOV-1998; 98ES-00002465.  
XX  
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
XX  
XX Ezquerro Saenz JI, Lasaarte Sagaribelza JU, Prieto Valtuena J;  
PI Borras Cuesta F;  
XX  
XX WPI; 2000-411935/35.  
XX  
XX Peptides that antagonise binding of transforming growth factor betaf,  
PT useful for treatment of liver disease, especially cirrhosis, are partial  
PT sequences of the factor or its receptors.  
XX  
XX Disclosure; Page 24; 86pp; Spanish.  
XX  
XX The invention relates to synthetic peptides that antagonise the binding  
CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in  
CC those which have partial amino acid sequences identical, or similar, with  
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
CC examples of the peptides of the invention. The peptides act by  
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
CC they are inhibitors of stimulation of collagen synthesis in liver cells  
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
CC expression systems) encoding the peptides are used for treatment of liver  
CC disease, specifically cirrhosis  
XX  
XX Sequence 23 AA;  
SQ  
Query Match 100.0%; Score 89; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FCLGCPYIWSLDT 14  
DB 10 FCLGCPYIWSLDT 23  
RESULT 5  
ID AAY92954  
AAV92954 standard; peptide; 23 AA.  
XX  
AC AAY92954;  
XX  
XX 08-NOV-2000 (first entry)  
XX  
XX Transforming growth factor inhibitory peptide #10.  
XX  
XX Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;  
KM competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KM extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
XX  
XX Homo sapiens.  
XX  
XX W0200031135-A1.  
XX  
XX 02-JUN-2000.  
XX  
XX 23-NOV-1999; 99WO-ES000375.  
XX  
XX 24-NOV-1998; 98ES-00002465.  
XX  
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
XX  
XX Ezquerro Saenz JI, Lasaarte Sagaribelza JU, Prieto Valtuena J;

PI Borras Cuesta F;  
XX  
XX WPI; 2000-411935/35.  
XX  
XX Peptides that antagonise binding of transforming growth factor betaf,  
PT useful for treatment of liver disease, especially cirrhosis, are partial  
PT sequences of the factor or its receptors.  
XX  
XX Claim 11; Page 82; 86pp; Spanish.  
XX  
XX The invention relates to synthetic peptides that antagonise the binding  
CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in  
CC vivo which have partial amino acid sequences identical, or similar, with  
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
CC examples of the peptides of the invention. The peptides act by  
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
CC they are inhibitors of stimulation of collagen synthesis in liver cells  
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
CC expression systems) encoding the peptides are used for treatment of liver  
CC disease, specifically cirrhosis  
XX  
XX Sequence 23 AA;  
SQ  
Query Match 100.0%; Score 89; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FCLGCPYIWSLDT 14  
DB 10 FCLGCPYIWSLDT 23  
RESULT 6  
ID ABU08659  
ABU08659 standard; peptide; 25 AA.  
XX  
XX ABU08659;  
XX  
XX 09-JUN-2003 (first entry)  
XX  
XX Human transforming growth factor (TGF)-beta 1 residues 41-65.  
XX  
XX Human; transforming growth factor beta 1; TGF-betaf;  
KM TGF-beta induced growth inhibition; TGF-beta receptor; binding inhibitor;  
KM mink lung epithelial cell; incimal hyperplasia; angioplasia;  
KM tissue fibrosis; glomerulonephritis.  
XX  
XX Homo sapiens.  
XX  
XX US6500920-B1.  
XX  
XX 31-DEC-2002.  
XX  
XX 11-JUN-1998; 98US-00095637.  
XX  
XX 19-JUN-1997; 97US-0050202P.  
XX  
XX (UYSL-) UNIV ST LOUIS.  
XX  
XX Haung JS;  
XX  
XX WPI; 2003-352187/33.  
XX  
XX New peptides of transforming growth factor-beta 1, 2 and 3 useful for  
PT inhibiting specific binding of TGF-beta to its receptor and for blocking  
PT TGF-beta induced growth inhibition of a cell.  
XX  
XX Claim 14; Fig 5B; 14pp; English.  
XX  
XX The invention describes a peptide (I) of at least 25 amino acids  
CC comprising amino acids 49-58 of transforming growth factor (TGF)-beta 2,  
CC amino acids 41-65 of TGF-beta 1, or amino acids 41-65 of TGF-beta 3

CC capable of blocking TGF-beta induced growth inhibition of a cell. The TGF  
 CC -beta 2 and TGF-beta 1 are also capable of inhibiting specific binding of  
 CC TGF-beta to TGF-beta receptor on a cell. The methods are useful for  
 CC inhibiting specific binding of a TGF-beta to a TGF-beta receptor on a  
 CC cell comprising contacting the cell with a peptide of 10-25 amino acids,  
 CC where: (a) the peptide comprises amino acids 49-58 of a TGF-beta 1 or  
 CC amino acids 49-58 of a TGF-beta 2; and (b) the peptide inhibits the  
 CC specific binding of a TGF-beta to a TGF-beta receptor on a cell. The  
 CC methods are also useful for blocking TGF-beta-induced growth inhibition  
 CC of a cell comprising contacting the cell with a peptide of at least 10  
 CC amino acids, as described above, in particular a milk lung epithelial  
 CC cell. The methods are also useful for blocking TGF-beta-induced growth  
 CC inhibition of a cell comprising contacting the cell with a peptide of at  
 CC least 25 amino acids, where: (a) the peptide comprises amino acids 41-65  
 CC of a TGF-beta 1, or amino acids 41-65 of a TGF-beta 2; and (b) the  
 CC peptide blocks TGF-beta-induced growth inhibition of the cell. The  
 CC peptides are useful in inhibiting, ameliorating or reversing the effects  
 CC of TGF-beta and treating diseases in which TGF-beta is associated such as  
 CC intimal hyperplasia, following angioplasty, tissue fibrosis and  
 CC glomerulonephritis. This is the amino acid sequence of human transforming  
 CC growth factor (TGF)-beta 1 residues 41-65

SO Sequence 25 AA;

Query Match 100.0%; Score 89; DB 6; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGCPYIWSLDT 14  
 |||||  
 Db 3 FCLGCPYIWSLDT 16

RESULT 7  
 ABM79533  
 ID ABM79533 standard; peptide; 25 AA.

AC ABM79533;  
 XX  
 DT 22-APR-2004 (first entry)

DE Human transforming growth factor betal peptide.

XX Human; TGF beta; transforming growth factor beta; antagonist;  
 KM cutaneous wound; burn; wound healing; vulnery; nephrotoxic;  
 KM ophthalmological; cytostatic; antiinflammatory; hepatotropic; cardiant.

XX Homo sapiens.

XX MO2003093293-A2.

XX 13-NOV-2003.

XX 15-APR-2003; 2003WO-US011437.

XX 29-APR-2002; 2002US-00135946.

XX (YUSL-) UNIV SAINT LOUIS.

XX Huang JS;

XX WPI; 2004-042374/04.

XX Inhibiting activity of transforming growth factor-beta useful for  
 PT treating wounds; cancer or fibrosis, comprises administering composition  
 PT comprising peptide antagonist of transforming growth factor-beta.

XX Claim 4; Fig 5B; ODP; English.

XX The present invention relates to a method of inhibiting activity of  
 CC transforming growth factor-beta (TGF-beta), which comprises administering  
 CC a composition comprising a non-naturally occurring peptide that binds to  
 CC a TGF-beta receptor, blocks the TGF-beta receptor from binding naturally

CC occurring TGF-beta and inhibits the activity of TGF-beta. The method can  
 CC be used for reducing scarring due to wounds, such as burns, scrapes,  
 CC puncture wounds and lacerations, promoting re-epithelialization of a  
 CC wound, reducing the deposition of an extracellular matrix protein in the  
 CC extracellular matrix and treating diseases mediated by TGF-beta activity,  
 CC particularly glomerulonephritis, macular degeneration, intimal  
 CC hyperplasia, cancer, fibrosis (e.g. scar formation, liver cirrhosis, and  
 CC kidney fibrosis), cystic fibrosis, lung fibrosis or heart fibrosis) and  
 CC respiratory distress syndrome. The present sequence is a fragment of the  
 CC human TGF betal protein

SO Sequence 25 AA;

Query Match 100.0%; Score 89; DB 8; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGCPYIWSLDT 14  
 |||||  
 Db 3 FCLGCPYIWSLDT 16

RESULT 8  
 AAR90828  
 ID AAR90828 standard; peptide; 50 AA.

AC AAR90828;

XX 25-MAR-2003 (revised)  
 DT 25-JAN-1980 (first entry)

DE Pre-transforming growth factor beta 1 residues 252 to 302.

XX transforming growth factor beta 1; wound healing; recombinant production.

XX Homo sapiens.

XX US5482851-A.

XX 09-JAN-1996.

XX 05-NOV-1993; 93US-00147364.

XX 22-MAR-1985; 85US-00715142.

XX 13-MAR-1987; 87US-00025423.

XX 04-AUG-1989; 89US-00389929.

XX 04-MAR-1992; 92US-00845893.

XX (GETH ) GENENTECH INC.

XX Goeddel DV, Derynck RMA;

XX WPI; 1996-076891/08.

XX N-PSDB; AAT15721.

XX New recombinant human transforming growth factor-beta prods. - produced  
 PT using Chinese hamster ovary cells, for use in diagnostic applications or  
 PT in therapy.

XX Example 2; Fig 2; 26pp; English.

XX The transforming growth factor (TGF) beta 1 exon (residues 252 to 302)  
 CC was identified using the "long probe" strategy used previously for TGF-  
 CC alpha. Long oligonucleotides (71572-23) designed on the basis of the  
 CC partial protein sequence were used as hybridisation probes for the exon  
 CC in a human genomic DNA library. The TGF beta 1 exon was then used as a  
 CC probe for the isolation of TGF beta 1 cDNA (see AAT15270). DNA encoding  
 CC TGF beta 1 is useful for the recombinant production of the protein, which  
 CC is useful in, e.g. wound healing. (Updated on 25-MAR-2003 to correct PF  
 CC field.)

XX Sequence 50 AA;

Query Match 100.0%; Score 89; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIMSLDT 14  
 |||||  
 DB 34 FCLGPCPYIMSLDT 47

RESULT 9  
 AAR04075  
 ID AAR04075 standard; protein, 51 AA.  
 XX AAR04075;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 31-OCT-2002 (revised)  
 DT 31-MAY-1989 (first entry)  
 XX  
 DE Sequence of genomic fragment encoding a TGF-beta 1 exon.  
 XX  
 XX Transforming growth factor beta-3 (TGF beta 3); tumour cells;  
 KM growth inhibition.  
 XX  
 XX Homo sapiens.  
 OS  
 XX W08912101-A.  
 PN  
 XX 14-DEC-1989.  
 PD  
 XX 08-JUN-1988; 88WO-US001945.  
 PF  
 XX 08-JUN-1988; 88WO-US001945.  
 XX  
 PR 08-JUN-1988; 88WO-US001945.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Derynck RMA, Goeddel DV;  
 PI  
 XX WPI; 1990-007474/01.  
 DR P-PSDB; AAR04075.  
 XX  
 XX Nucleotide sequence encoding transforming growth factor beta-3 - used as  
 PT a probe, or to produce tgf beta-3, for growth inhibition of certain  
 PT normal and neoplastic cells, e.g. A549.  
 XX  
 XX Disclosure; Fig 2; 61pp; English.  
 PS  
 XX This sequence encodes an exon of transforming growth factor-beta 1 (TGF-  
 CC beta 1) polypeptide corresponding to AA's 288-338 of mature TGF-beta 1.  
 CC The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-  
 CC beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and  
 CC neoplastic cell growth inhibition. (Updated on 31-OCT-2002 to add missing  
 CC OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-  
 CC MAR-2003 to correct PI field.)  
 CC  
 XX Sequence 51 AA;  
 SQ

Query Match 100.0%; Score 89; DB 2; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIMSLDT 14  
 |||||  
 DB 34 FCLGPCPYIMSLDT 47

RESULT 10  
 AAW78788  
 ID AAW78788 standard; protein, 51 AA.  
 XX AAW78788;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT

DT 21-DEC-1998 (first entry)  
 XX  
 XX Human transforming growth factor-beta fragment (aa288-338).  
 DE  
 XX Transforming growth factor-beta 1; TGF-beta 1; human.  
 KM  
 XX Homo sapiens.  
 OS  
 XX U55801231-A.  
 PN  
 XX 01-SEP-1998.  
 PD  
 XX 30-MAY-1995; 95US-00454468.  
 PF  
 XX 22-MAR-1985; 85US-00715142.  
 PR 13-MAR-1987; 87US-00025423.  
 PR 04-AUG-1989; 89US-00389929.  
 PR 04-MAR-1992; 92US-00845893.  
 PR 05-NOV-1993; 93US-00147364.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Derynck RMA, Goeddel DV;  
 PI  
 XX WPI; 1998-494840/42.  
 DR N-PSDB; AAV52936.  
 DR  
 XX DNA encoding transforming growth factor-beta precursor sequence - useful  
 PT for analysis to perform manipulations to increase yield of recombinant  
 PT production of the protein.  
 XX  
 XX Example 2; Fig 2; 26pp; English.  
 PS  
 XX This polypeptide comprises amino acid residues 288-338 of human  
 CC transforming growth factor-beta 1 precursor (preTGF-beta 1, see also  
 CC AAW78785). It is encoded by an isolated fragment (see AAV52936) of the  
 CC TGF-beta 1 gene. The invention relates to the recombinant production of  
 CC TGF-beta. Nucleic acid encoding TGF-beta have been isolated and cloned  
 CC into vectors which are replicated in bacteria and expressed in eukaryotic  
 CC cells. TGF-beta recovered from transformed cells is used in known  
 CC therapeutic applications. (Updated on 25-MAR-2003 to correct PR field.)  
 CC  
 XX Sequence 51 AA;  
 SQ

Query Match 100.0%; Score 89; DB 2; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYIMSLDT 14  
 |||||  
 DB 34 FCLGPCPYIMSLDT 47

RESULT 11  
 ABB43879  
 ID ABB43879 standard; peptide, 51 AA.  
 XX ABB43879;  
 AC  
 XX 04-FEB-2002 (first entry)  
 DT  
 XX Peptide #11385 encoded by human foetal liver single exon probe.  
 DE  
 XX Human; foetal liver; gene expression; single exon nucleic acid probe.  
 KM  
 XX Homo sapiens.  
 OS  
 XX W0200157277-A2.  
 PN  
 XX 09-AUG-2001.  
 PD  
 XX 30-JAN-2001; 2001WO-US000669.  
 PF  
 XX

PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483447/52.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human fetal liver.  
XX  
PS Claim 27; SEQ ID NO 36514; 639bp + Sequence Listing; English.  
XX  
CC The invention relates to a single exon nucleic acid probe for measuring  
CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human fetal liver. The  
CC present sequence is a peptide encoded by a single exon nucleic acid probe  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 51 AA;  
XX  
Query Match 100.0%; Score 89; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 FCLGPCPYWISLDT 14  
Db |||||  
34 FCLGPCPYWISLDT 47  
XX  
RESULT 12  
AAM37799  
ID AAM37799 standard; protein; 51 AA.  
XX  
AC AAM37799;  
XX  
DT 17-OCT-2001 (first entry)  
XX  
DE Peptide #11836 encoded by probe for measuring placental gene expression.  
XX  
XX Probe; microarray; human; placenta; antenatal diagnosis;  
KM genetic disorder.  
XX  
OS Homo sapiens.  
XX  
XX WO200157272-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 30-JUN-2000; 2000US-00608408.  
XX 03-AUG-2000; 2000US-00632366.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488897/53.  
XX  
XX

XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human placenta.  
XX  
XX Claim 27; SEQ ID NO 38068; 654bp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes (SEQ:  
CC see A113115-A157546). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for producing a microarray for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders  
XX  
XX  
SQ Sequence 51 AA;  
XX  
Query Match 100.0%; Score 89; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 FCLGPCPYWISLDT 14  
Db |||||  
34 FCLGPCPYWISLDT 47  
XX  
RESULT 13  
AAM77605  
ID AAM77605 standard; protein; 51 AA.  
XX  
XX AAM77605;  
XX  
XX 06-NOV-2001 (first entry)  
XX  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37911.  
XX  
XX Human bone marrow expressed exon; gene expression analysis; probe;  
KW microarray; cancer; leukaemia; lymphoma; myeloma.  
XX  
XX Homo sapiens.  
XX  
XX WO200157276-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000668.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 30-JUN-2000; 2000US-00608408.  
XX 03-AUG-2000; 2000US-00632366.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488900/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human bone marrow.  
XX  
XX Example 4; SEQ ID NO 37911; 658bp + Sequence Listing; English.  
XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
CC protein encoded by one of the probes of the invention  
XX  
XX  
SQ Sequence 51 AA;  
XX



[illegible]

CC	comprising (a) identifying exons from genomic sequence by the method
CC	above and (b) measuring the expression of each of the exons in several
CC	tissues and/or cell types using hybridisation to a single exon
CC	microarrays having a probe with the exon, where a common pattern of
CC	expression of the exons in the tissues and/or cell types indicates that
CC	the exons should be assigned to a single gene; a peptide comprising one
CC	of 1201 sequences, mentioned in the specification, or encoded by the
CC	probe/open reading frames (ORF). The probes are used for gene expression
CC	analysis, and for identifying exons in a gene, particularly using human
CC	lung derived mRNA and for the study of lung diseases such as asthma, lung
CC	cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC	disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC	tuberosc sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC	Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC	histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC	Karsagenier syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC	dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC	present sequence is a peptide/protein encoded by a single exon probe of
CC	the invention. Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic format
CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
CC	
SQ	Sequence 51 AA;
Query Match	100.0%; Score 89; DB 5; Length 51;
Best Local Similarity	100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0
CY	1 FCTGSPCPYWSLDT 14 
Db	34 FCLGSPCPYWSLDT 47 
RESULT 15	
AAB68685	AAB68685 standard; protein, 60 AA.
XX	
AC	AAB68685;
XX	
DT	03-MAY-2001 (first entry)
XX	
DE	Human TGFbeta1 protein #1.
KM	Human; transforming growth factor beta2; TGFbeta2; SREX;
KW	systemic evolution of ligands by exponential enrichment.
XX	
OS	Homo sapiens.
XX	
PN	WO200109156-A1.
PD	08-FEB-2001.
PF	26-JUL-2000; 2000WO-US020397.
PR	29-JUL-1999; 99US-00363939.
PA	(NEXS-) NEXSTAR PHARM INC.
PI	Pagratris N, Lochrie M, Gold L;
DR	WPI; 2001-218217/22.
PT	New RNA ligand to human transforming growth factor beta2, useful as
PS	pharmaceuticals, diagnostics and as immunochemical reagents.
XX	
XX	Disclosure; Page 71; 178pp; English.
XX	
XX	The present invention relates to non-naturally occurring, high-affinity
XX	RNA ligands to human transforming growth factor beta2 (TGFbeta2). The
XX	oligonucleotide ligands were identified by the SREX method (SREX stands
XX	for Systemic Evolution of Ligands by Exponential Enrichment). The
XX	oligonucleotide ligands are useful in any process in which binding to
XX	TGFbeta2 is required. The ligands may be useful as pharmaceuticals,

CC diagnostics, imaging agents and immunohistochemical reagents  
XX  
SQ Sequence 60 AA;

Query Match 100.0%; Score 89; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 3.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPPYIWSLDT 14  
|||||  
Db 43 FCLGPPYIWSLDT 56

Search completed: June 14, 2005, 15:46:23  
Job time : 80.2308 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2005, 15:35:40 ; Search time 15.6154 Seconds  
(without alignments)  
86.263 Million cell updates/sec

Title: US-09-831-253F-2  
Perfect score: 89  
Sequence: 1 FCLGCPYIWSLDT 14

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	130	2	I48196 transforming growt
2	89	100.0	315	2	A40057 transforming growt
3	89	100.0	390	1	WPHU2 transforming growt
4	89	100.0	390	1	WPHU2 transforming growt
5	89	100.0	390	1	WPHU2 transforming growt
6	89	100.0	390	2	A26960 transforming growt
7	89	100.0	390	2	JC4023 transforming growt
8	89	100.0	390	2	A27512 transforming growt
9	89	100.0	390	2	I46463 transforming growt
10	89	100.0	390	2	S10219 transforming growt
11	89	100.0	390	2	S01413 transforming growt
12	82	92.1	373	2	A41918 transforming growt
13	75	84.3	382	2	B61036 transforming growt
14	68	76.4	112	2	A61439 transforming growt
15	68	76.4	412	2	A39489 transforming growt
16	68	76.4	413	1	WFXLB2 transforming growt
17	68	76.4	414	1	WFXLB2 transforming growt
18	68	76.4	414	1	WFXLB2 transforming growt
19	68	76.4	414	2	B31249 transforming growt
20	68	76.4	414	2	B31249 transforming growt
21	62	69.7	410	2	S01825 transforming growt
22	62	69.7	410	2	A41397 transforming growt
23	62	69.7	412	2	A34939 transforming growt
24	61	68.5	410	2	A36169 transforming growt
25	48	51.7	768	2	A55706 transforming growt
26	46	49.4	433	2	D68017 hypothetical prote
27	44	49.4	433	2	B90288 chlamn biosynthes
28	44	49.4	433	2	H90359 insulin receptor p
29	44	49.4	1382	1	INHUR

30	43	48.3	695	2	S66662 protein-glutamine
31	43	48.3	1372	2	A34157 insulin receptor p
32	43	48.3	1383	2	A36080 insulin receptor p
33	42	47.2	157	2	S14021 hypothetical prote
34	42	47.2	239	2	G64924 ntic protein homol
35	42	47.2	239	2	F85774 probable oxidoredu
36	42	47.2	239	2	B90926 hypothetical prote
37	42	47.2	549	2	T33517 organic cation tra
38	42	47.2	556	2	S50862 membrane transport
39	42	47.2	567	2	A33974 protein RL1G1.4
40	41	46.1	274	2	C88931 probable ferredoxi
41	41	46.1	366	2	G82970 hypothetical prote
42	41	46.1	398	2	G90225 probable oxygen-in
43	41	46.1	399	2	C71728 oxygen-inde
44	41	46.1	404	2	AE3473 alpha-glucosidase
45	41	46.1	864	2	JC4624

## ALIGNMENTS

## RESULT 1

I48196 transforming growth factor beta-1 precursor - golden hamster (fragment)  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 02-Jul-1996 #sequence\_revision 04-Oct-1996 #text\_change 09-Jul-2004  
C:Accession: I48196  
R:Wong, D.T.; Donoff, R.B.; Yang, J.; Song, B.Z.; Matossian, K.; Nagura, N.; Elovic, A.;  
Am. J. Pathol. 143, 130-142, 1993  
A:Title: Sequential expression of transforming growth factors alpha and beta 1 by eosino-  
A:Reference number: I48196; MUID:93304479; PMID:8317544  
A:Accession: I48196  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-130 <RES>  
A:Cross-references: UNIPROT:Q08714; EMBL:X60296; NID:9396177; PIDN:CAA42838.1; PID:93961  
C:Superfamily: inhibin

## Query Match

Best Local Similarity 100.0%; Score 89; DB 2; Length 130;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGCPYIWSLDT 14  
DB 61 FCLGCPYIWSLDT 74

## RESULT 2

A40057 transforming growth factor beta-1 precursor - bovine (fragment)  
N:Alternate names: beta-RGF; cartilage-inducing factor-A; BGF-dependent TGF or dBGf; MGF  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 09-Jul-2004  
C:Accession: A40057; A42320; A05284; A24322; B61439  
R:Van Oosbergen-Schilling, E.; Kondaiah, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.  
Mol. Endocrinol. 1, 693-698, 1987  
A:Title: Complementary deoxyribonucleic acid cloning of bovine transforming growth facto  
A:Reference number: A40057; MUID:91042552; PMID:3153455  
A:Accession: A40057  
A:Molecule type: mRNA  
A:Residues: 1-315 <VAN>  
A:Cross-references: UNIPROT:P18341; GB:M6271; NID:9163747; PIDN:AAA30778.1; PID:9163748  
R:Ogawa, Y.; Schmidt, D.K.; Daesch, J.R.; Chang, R.U.; Glaeser, C.B.  
J. Biol. Chem. 267, 2325-2328, 1992  
A:Title: Purification and characterization of transforming growth factor-beta2.3 and -be  
A:Reference number: A42320; MUID:92129307; PMID:1733936  
A:Accession: A42320  
A:Molecule type: protein  
A:Residues: 204-209, 'X', 211-217 <OGA>  
R:Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan, Y.C.E.; Stei  
Biochemistry 22, 5692-5698, 1983  
A:Title: Purification and properties of a type beta transforming growth factor from bovi  
A:Reference number: A05284; MUID:84104793; PMID:6607069

A:Accession: A05284  
A:Molecule type: protein  
A:Residues: 204-218 <ROB>  
R:Sevedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti, A.; Sie  
J. Biol. Chem. 261, 5693-5695, 1986  
A:Title: Cartilage-inducing factor-A. Apparent identity to transforming growth factor-b  
A:Reference number: A24322; MUID:86195954; PMID:3754555  
A:Accession: A24322  
A:Molecule type: protein  
A:Residues: 204-233 <SEY>  
R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.  
J. Protein Chem. 10, 565-575, 1991  
A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta  
A:Reference number: A61439; MUID:92189724; PMID:1799413  
A:Accession: B61439  
A:Molecule type: protein  
A:Residues: 204-209 'X', 211-217, 'XX', 220-232 <JIN>  
C:Comment: This polypeptide is composed of two polypeptide chains cross-linked by disulf  
C:Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogenic a  
ion. Cells grown in monolayer do not respond in a similar manner to these growth factors  
C:Superfamily: Inhibin  
C:Keywords: glycoprotein; growth factor; heterodimer  
F:204-315/Product: transforming growth factor beta-1 #status experimental <MAT>  
F:7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 100.0%; Score 89; DB 2; Length 315;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FCLGPCPYIWSLDT 14  
Db 246 FCLGPCPYIWSLDT 259  
RESULT 3  
WFM2  
transforming growth factor beta-1 precursor [validated] - human  
N:Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1986 #sequence revision 19-Oct-1995 #text\_change 09-Jul-2004  
C:Accession: A27513; A01395; A22290; I59664; S53444  
R:Derynck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.  
Nucleic Acids Res. 15, 3188-3189, 1987  
A:Title: Intron-exon structure of the human transforming growth factor-beta precursor ge  
A:Reference number: A27513; MUID:87174845; PMID:3470709  
A:Accession: A27513  
A:Molecule type: DNA  
A:Residues: 1-390 <DER>  
A:Cross-references: UNIPROT:P01137; GB:X05839; GB:Y00112; NID:G37097; PIDN:CAA29283.1; F  
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assefian, R.K.; Robert  
Nature 316, 701-705, 1985  
A:Title: Human transforming growth factor-beta complementary DNA sequence and expression  
A:Reference number: A01395; MUID:85296301; PMID:3861940  
A:Accession: A01395  
A:Molecule type: mRNA  
A:Residues: 1-3, 'P', 11-24, 'P', 26-159, 'R', 160-390 <DE2>  
A:Cross-references: GB:X05812; GB:J05114; NID:G37092; PIDN:CAA26580.1; PID:G37093  
A:Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a  
R:Massagué, J.; Like, B.  
J. Biol. Chem. 260, 2636-2645, 1985  
A:Title: Cellular receptors for type beta transforming growth factor. Ligand binding and  
A:Reference number: A22290; MUID:85131019; PMID:2982829  
A:Accession: A22290  
A:Molecule type: protein  
A:Residues: 279-295 'XX', 298-301 <MAS>  
R:Urushizaki, Y.; Nitsu, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.; Urushizaki,  
Tumor Res. 22, 41-55, 1987  
A:Title: Cloning and expression of the gene for human transforming growth factor-beta in  
A:Reference number: I59664  
A:Accession: I59664  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 279-390 <RES>

A:Cross-references: GB:M38449; NID:G339557; PIDN:AAA36735.1; PID:G339558  
R:Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyo, D.; Chait, B.T.; Marshak, D.R.,  
Biochem. J. 305, 87-92, 1995  
A:Title: Physical and biological characterization of a growth-inhibitory activity purified  
A:Reference number: S53444; MUID:95126934; PMID:7826358  
A:Accession: S53444  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 279-297 <STA>  
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide  
C:Genetics:  
A:Gene: GDB:TGFB1; TGFB  
A:Cross-references: GDB:120729; OMIM:190180  
A:Map position: 19q13.2-19q13.2  
C:Superfamily: Inhibin  
C:Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-278/Domain: propeptide #status predicted <PRO>  
F:244-246/Region: cell attachment (R-G-D) motif  
F:279-390/Product: transforming growth factor beta-1 #status experimental <MAT>  
F:182,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 100.0%; Score 89; DB 1; Length 390;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FCLGPCPYIWSLDT 14  
Db 321 FCLGPCPYIWSLDT 334  
RESULT 4  
WFM2  
transforming growth factor beta-1 precursor - mouse  
N:Alternate names: TGF type 2; TGF-beta  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text\_change 09-Jul-2004  
C:Accession: A01396  
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.  
J. Biol. Chem. 261, 4377-4379, 1986  
A:Title: The murine transforming growth factor-beta precursor.  
A:Reference number: A01396; MUID:86168129; PMID:3007454  
A:Accession: A01396  
A:Molecule type: mRNA  
A:Residues: 1-390 <DER>  
A:Cross-references: UNIPROT:P04202; GB:M13177; NID:G201952; PIDN:AAA40423.1; PID:G201953  
A:Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a  
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide  
C:Superfamily: Inhibin  
C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen; transform  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-278/Domain: propeptide #status predicted <PRO>  
F:244-246/Region: cell attachment (R-G-D) motif  
F:279-390/Product: transforming growth factor beta-1 #status predicted <MAT>  
F:182,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 89; DB 1; Length 390;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 FCLGPCPYIWSLDT 14  
Db 321 FCLGPCPYIWSLDT 334  
RESULT 5  
A26960  
transforming growth factor beta-1 precursor - green monkey  
C:Species: Cercopithecus aethiops (green monkey, grivet)  
C:Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text\_change 09-Jul-2004  
A:Accession: A26960  
R:Sharples, K.; Ploeman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.  
DNA 6, 239-244, 1987

A:Title: Cloning and sequence analysis of simian transforming growth factor-beta cDNA.  
A:Reference number: A26960; MUID:87246074; PMID:3474130  
A:Accession: A26960  
A:Molecule type: mRNA  
A:Residues: 1-390 <SHA>  
A:Cross-references: UNIPROT:P09533; GB:M16658; NID:G176552; PIDN:AAA5369.1; PID:G176553  
C:Superfamily: inhibin  
C:Keywords: growth factor  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-390/Product: transforming growth factor beta #status predicted <MAT>

Query Match 100.0%; Score 89; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGCPYIWSLDT 14  
Db 321 FCLGCPYIWSLDT 334

RESULT 6  
JC4023  
transforming growth factor beta-1 - dog  
C:Species: Canis lupus familiaris (dog)  
C:Date: 13-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: JC4023  
R:Manning, A.M.; Auchampach, J.A.; Drong, R.F.; Slightom, J.L.  
Gene 155, 307-308, 1995  
A:Title: Cloning of a canine cDNA homologous to the human transforming growth factor-beta  
A:Reference number: JC4023; MUID:95237630; PMID:7721110  
A:Accession: JC4023  
A:Molecule type: mRNA  
A:Residues: 1-390 <MAN>  
A:Cross-references: UNIPROT:P54831; GB:L34956; NID:G516071; PIDN:AAA51458.1; PID:G516072  
C:Comment: This factor plays a multifunctional role as a regulator of mammalian cell growth  
C:Genetics:  
A:Gene: tgf-beta1  
C:Superfamily: inhibin  
C:Keywords: growth factor; transforming protein  
F:288-390/Product: transforming growth factor beta 1 #status predicted <MAT>

Query Match 100.0%; Score 89; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGCPYIWSLDT 14  
Db 321 FCLGCPYIWSLDT 334

RESULT 7  
A27512  
transforming growth factor beta-1 precursor - pig  
N:Alternate names: TGF-beta  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 09-Jul-2004  
C:Accession: A27512; A26356; I46657  
R:Derynck, R.; Rhee, L.  
Nucleic Acids Res. 15, 3187, 1987  
A:Title: Sequence of the porcine transforming growth factor-beta precursor.  
A:Reference number: A27512; MUID:87174844; PMID:3470708  
A:Accession: A27512  
A:Molecule type: mRNA  
A:Residues: 1-390 <DER>  
A:Cross-references: UNIPROT:P07200  
R:Chelifer, S.; Weatherbee, J.A.; Tang, M.L.S.; Anderson, J.K.; Mole, J.E.; Lucas, R.; Cell 48, 409-415, 1987  
A:Title: The transforming growth factor-beta system, a complex pattern of cross-reactive  
A:Reference number: A90890; MUID:87102890; PMID:2879635  
A:Accession: A26356  
A:Molecule type: protein  
A:Residues: 279-322 <CR>  
R:Kondaiah, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn, M.B.; Robert

J. Biol. Chem. 263, 18313-18317, 1988  
A:Title: cDNA cloning of porcine transforming growth factor-beta 1 mRNA. Evidence for a  
A:Reference number: I46657; MUID:89054010; PMID:2461367  
A:Accession: I46657  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-390 <KON>  
A:Cross-references: GB:M23703; NID:G755044; PIDN:AAA64616.1; PID:G755045  
C:Genetics:  
A:Gene: TGF-beta-1  
C:Superfamily: inhibin  
C:Keywords: growth factor

Query Match 100.0%; Score 89; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGCPYIWSLDT 14  
Db 321 FCLGCPYIWSLDT 334

RESULT 8  
I46463  
transforming growth factor beta-1 - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 19-Dec-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: I46463; S45115  
R:Woodall, C.J.; McLaren, L.J.; Watt, N.U.  
Gene 150, 371-373, 1994  
A:Title: Sequence and chromosomal localization of the gene encoding ovine latent transfo  
A:Reference number: I46463; MUID:95121932; PMID:7821809  
A:Accession: I46463  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-390 <MO>  
A:Cross-references: UNIPROT:P50414; EMBL:X76916; NID:G496648; PIDN:CAA54242.1; PID:G4966  
C:Note: submitted to the EMBL Data Library, December 1993  
C:Superfamily: inhibin

Query Match 100.0%; Score 89; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCLGCPYIWSLDT 14  
Db 321 FCLGCPYIWSLDT 334

RESULT 9  
S10219  
transforming growth factor beta-1 precursor - rat  
N:Alternate names: TGF type 2; TGF-beta  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
C:Accession: S10219; PT0023; S02267  
R:Qian, S.W.; Kondaiah, P.; Roberts, A.B.; Sporn, M.B.  
Nucleic Acids Res. 18, 3059, 1990  
A:Title: cDNA cloning by PCR of rat transforming growth factor-beta-1.  
A:Reference number: S10219; MUID:90272425; PMID:2349108  
A:Accession: S10219  
A:Molecule type: mRNA  
A:Residues: 1-390 <QIA>  
A:Cross-references: UNIPROT:P17246; EMBL:X52498; NID:G57341; PIDN:CAA36741.1; PID:G57342  
R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.  
J. Biochem. 106, 304-310, 1989  
A:Title: Purification and structural analysis of a latent form of transforming growth fa  
A:Reference number: PT0023; MUID:90036779; PMID:2478527  
A:Accession: PT0023  
A:Molecule type: protein  
A:Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 <OKA>  
R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.  
FEBS Lett. 242, 240-244, 1989

A;Title: One of two subunits of masking protein in latent TGF-beta is a part of pro-TGF-  
A;Accession: S02267; MUID:89121078; PMID:2914605  
A;Molecule type: protein  
A;Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 <OK>  
C;Superfamily: inhibin  
C;Keywords: glycoprotein; growth factor; integrin binding  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-278/Domain: propeptide #status experimental <PRO>  
F;244-246/Region: cell attachment (R-G-D) motif  
F;229-190/Product: transforming growth factor beta-1 #status predicted <MAT>  
F;82,116,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 89; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGCPYIWSLDT 14  
Db 321 FCLGCPYIWSLDT 334

RESULT 10  
S01413  
transforming growth factor beta-1 precursor - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C;Accession: S01413  
R;Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.  
Nucleic Acids Res. 16, 8730, 1988  
A;Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1).  
A;Reference number: S01413; MUID:88335639; PMID:3166520  
A;Accession: S01413  
A;Molecule type: DNA  
A;Residues: 1-391 <JUK>  
A;Cross-references: UNIPROT:P07200; EMBL:X12373; NID:963808; PIDN:CAA30933.1; PID:963808  
C;Superfamily: inhibin  
C;Keywords: growth factor

Query Match 100.0%; Score 89; DB 2; Length 391;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGCPYIWSLDT 14  
Db 322 FCLGCPYIWSLDT 335

RESULT 11  
A41918  
transforming growth factor beta-4 precursor - chicken (fragment)  
N;Alternate names: TGF-beta 4  
C;Species: Gallus gallus (chicken)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: A41918; A34941; S03110  
R;Burt, D.W.; Jakowlew, S.B.  
Mol. Endocrinol. 6, 989-992, 1992  
A;Title: Correction: a new interpretation of a chicken transforming growth factor-beta 4  
A;Reference number: A41918; MUID:92357039; PMID:1355860  
A;Accession: A41918  
A;Molecule type: mRNA  
A;Residues: 1-373 <BU>  
A;Cross-references: UNIPROT:P09531; GB:M31160; GB:X08012; GB:S41706; NID:91262437; PIDN:  
A;Note: sequence extracted from NCBI backbone (NCBI:110186, NCBI:P:110187)  
A;Note: this report corrects and reinterprets the sequence from reference A34941  
R;Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.  
Mol. Endocrinol. 2, 1186-1195, 1988  
A;Title: Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid enc  
A;Reference number: A34941; MUID:89112198; PMID:2464131  
A;Accession: A34941  
A;Molecule type: mRNA  
A;Residues: 'MDPMISIGPSCGSGSPWRPPTGTA'PWSIGSRRAATNASSCSTSSRYRAVGGRAI', 122-209, 'D', 211-373 <  
A;Cross-references: EMBL:X08012

A;Note: this sequence has been corrected in A41918  
C;Superfamily: inhibin  
C;Keywords: glycoprotein; growth factor  
F;1/Domain: signal sequence (fragment) #status predicted <SIG>  
F;223-225/Region: cell attachment (R-G-D) motif  
F;260-373/Product: transforming growth factor beta-4 #status predicted <MAT>  
F;54,109,153/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.1%; Score 82; DB 2; Length 373;  
Best Local Similarity 85.7%; Pred. No. 6.4e-05;  
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FCLGCPYIWSLDT 14  
Db 304 FCMGCPYIWSADT 317

RESULT 12  
B61036  
transforming growth factor beta-5 precursor - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 31-Dec-1993 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C;Accession: A34929; B61036  
R;Kondaliah, P.; Sande, M.J.; Smith, J.M.; Fields, A.; Roberts, A.B.; Sporn, M.B.; Melton,  
J. Biol. Chem. 265, 1089-1093, 1990  
A;Title: Identification of a novel transforming growth factor-beta (TGF-beta5) mRNA in X  
A;Reference number: A34929; MUID:90110090; PMID:2295601  
A;Accession: A34929  
A;Molecule type: mRNA  
A;Residues: 1-382 <KON>  
A;Cross-references: UNIPROT:P16176; GB:J05180; NID:9214821; PIDN:AAA49968.1; PID:9214822  
R;Roberts, A.B.; Ross, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Redbert, M.L.; Kond  
Growth Factors 2, 135-147, 1990  
A;Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium conditions  
A;Reference number: A61036; MUID:90255806; PMID:2340184  
A;Accession: B61036  
A;Molecule type: protein  
A;Residues: 271-276, 'X', 278-284, 'XX', 287-299 <ROB>  
C;Superfamily: inhibin  
C;Keywords: growth factor

Query Match 84.3%; Score 75; DB 2; Length 382;  
Best Local Similarity 78.6%; Pred. No. 0.00073;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FCLGCPYIWSLDT 14  
Db 313 YCLGNCPYIWSMDT 326

RESULT 13  
A61439  
transforming growth factor beta-2 - bovine  
N;Alternate names: cartilage-inducing factor B; MGF-a; milk growth factor a  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: A61439; A25485; B42320; S15389  
R;Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.  
J. Protein Chem. 10, 565-575, 1991  
A;Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta2  
A;Reference number: A61439; MUID:92189724; PMID:1799413  
A;Accession: A61439  
A;Molecule type: protein  
A;Residues: 1-112 <JIN>  
A;Cross-references: UNIPROT:P21214  
A;Experimental source: milk  
R;Seyedin, S.M.; Segarini, P.R.; Rosen, D.M.; Thompson, A.Y.; Bentz, H.; Graycar, J.  
J. Biol. Chem. 262, 1946-1949, 1987  
A;Title: Cartilage-inducing factor-B is a unique protein structurally and functionally re  
A;Reference number: A25485; MUID:87137406; PMID:3469199  
A;Accession: A25485  
A;Molecule type: protein

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A;Residues: 1-30 <SEX>
A;Experimental source: Bone
R;Ogawa, Y.; Schmidt, D.K.; Daech, J.R.; Chang, R.J.; Glaeser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A;Title: Purification and characterization of transforming growth factor-beta2.3 and -b2
A;Reference number: A42330; MUID:92129307; PMID:1733936
A;Accession: B42320
A;Molecule type: protein
A;Residues: 1-6, 'X', 8-14, 'XX', 17-34 <OGA>
A;Experimental source: bone
R;Cox, D.A.; Buerk, R.R.
Eur. J. Biochem. 197, 353-358, 1991
A;Title: Isolation and characterization of milk growth factor, a transforming-growth-fac
A;Reference number: S15389; MUID:91224126; PMID:2026157
A;Accession: S15389
A;Molecule type: protein
A;Residues: 1-16, 'XX', 19 <COX>
A;Experimental source: milk
C;Superfamily: inhibin
C;Keywords: growth factor; growth regulation; heterodimer; homodimer

Query Match          76.4%; Score 68; DB 2; Length 112;
Best Local Similarity 71.4%; Pred. No. 0.0028;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1  FCLGPCPYWMSLDT 14
DB      43  FCAGACPYLWMSDT 56

RESULT 14
A39489
transforming growth factor beta-2 precursor - chicken
N;Alternate names: TGF-beta2
C;Species: Gallus gallus (chicken)
C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: A39489; A61018; S25849
R;Burt, D.W.; Paton, I.R.
DNA Cell Biol. 10, 723-734, 1991
A;Title: Molecular cloning and primary structure of the chicken transforming growth fac
A;Reference number: A39489; MUID:92075163; PMID:1683775
A;Accession: A39489
A;Molecule type: DNA
A;Residues: 1-412 <BUR>
A;Cross-references: UNIPROT:P30371; GB:X58071; NID:963810; PIDD:CAA41101.1; PID:9833616;
R;Jukowlew, S.B.; Dillard, P.J.; Sporn, W.B.; Roberts, A.B.
Growth Factors 2, 123-133, 1990
A;Title: Complementary deoxyribonucleic acid cloning of an mRNA encoding transforming gr
A;Reference number: A61018; MUID:90253805; PMID:2340183
A;Accession: A61018
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-94, 'G', 96-244, 'L', 246-412 <JAK>
C;Genetics:
A;Introns: 115/1; 169/3; 214/1; 251/1; 309/2; 360/3
C;Superfamily: inhibin
C;Keywords: growth factor; growth regulation; mitogen; transformation
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-300/Domain: propeptide #status predicted <PRO>
F;301-412/Product: transforming growth factor beta-2 #status predicted <MAT>

Query Match          76.4%; Score 68; DB 2; Length 412;
Best Local Similarity 71.4%; Pred. No. 0.0088;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1  FCLGPCPYWMSLDT 14
DB      343  FCAGACPYLWMSDT 356

RESULT 15
WFXLB2
transforming growth factor beta-2 precursor - African clawed frog

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C;Species: Xenopus laevis (African clawed frog)
C;Date: 12-Feb-1993 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: S09510; A61036
R;Rebert, M.L.; Bhatia-Dey, N.; Dawid, I.B.
Nucleic Acids Res. 18, 2185, 1990
A;Title: The sequence of TGF-beta2 from Xenopus laevis.
A;Reference number: S09510; MUID:90245678; PMID:2336403
A;Accession: S09510
A;Molecule type: mRNA
A;Residues: 1-413 <REB>
A;Cross-references: UNIPROT:P17247; EMBL:X51817; NID:9414789; PIDD:CAA36116.1; PID:95513
R;Roberts, A.B.; Rosa, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Rebert, M.L.; Kond.
Growth Factors 2, 135-147, 1990
A;Title: Isolation and characterization of TGF-beta2 and TGF-betas from medium condition.
A;Reference number: A61036; MUID:90253806; PMID:2340184
A;Accession: A61036
A;Molecule type: protein
A;Residues: 302-307, 'X', 309-315, 'XX', 318-319 <ROB>
C;Superfamily: inhibin
C;Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-301/Domain: propeptide #status predicted <PRO>
F;302-413/Product: transforming growth factor beta-2 #status predicted <MAT>
F;72,140,241/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          76.4%; Score 68; DB 1; Length 413;
Best Local Similarity 71.4%; Pred. No. 0.0088;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1  FCLGPCPYWMSLDT 14
DB      344  FCAGACPYLWMSDT 357

Search completed: June 14, 2005, 15:52:10
Job time : 16.6154 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 14, 2005, 15:34:23 ; Search time 74.8462 Seconds

(without alignments)  
95.785 Million cell updates/sec

Title: US-09-831-253F-2

Perfect score: 89

Sequence: 1 FCLGCPYIWSLDT 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	50	2 Q28240	Q28240 cervus elap
2	89	100.0	51	2 Q72487	Q72487 homo sapien
3	89	100.0	78	2 Q70316	Q70316 sus scrofa
4	89	100.0	112	2 Q02730	Q02730 oryctolagus
5	89	100.0	124	2 Q95N80	Q95N80 canis faml1
6	89	100.0	130	2 Q08714	Q08714 mesocricetu
7	89	100.0	315	1 TGFI_BOVIN	P18341 bos taurus
8	89	100.0	368	2 Q8R4D9	Q8R4D9 simodon hi
9	89	100.0	390	1 TGFI_CANFA	P54831 canis faml1
10	89	100.0	390	1 TGFI_CANVO	Q921y6 cavia porce
11	89	100.0	390	1 TGFI_CERAE	P09533 cercopithec
12	89	100.0	390	1 TGFI_HORSE	O15011 equus cabal
13	89	100.0	390	1 TGFI_HUMAN	P01137 homo sapien
14	89	100.0	390	1 TGFI_MOUSE	P04202 mus musculu
15	89	100.0	390	1 TGFI_PIG	P07200 sus scrofa
16	89	100.0	390	1 TGFI_RAT	P17246 rattus norv
17	89	100.0	390	1 TGFI_SHEEP	P50414 ovis aries
18	89	100.0	390	2 Q9TUM6	Q9TUM6 equus cabal
19	89	92.1	101	2 Q9RI84	Q9RI84 meriones un
20	82	92.1	373	1 TGFI_CHICK	P09531 gallus gall
21	75	84.3	382	1 TGFI_XENIA	P16176 xenopus lae
22	69	77.5	62	2 Q90YF4	Q90YF4 pleuronecte
23	69	77.5	77	2 Q90YF8	Q90YF8 oncorhynch
24	69	77.5	88	2 Q90YF7	Q90YF7 oncorhynch
25	69	77.5	91	2 Q9MYZ1	Q9MYZ1 capra hircu
26	69	77.5	361	2 Q98854	Q98854 cyprinus ca
27	69	77.5	411	2 Q7SZV4	Q7SZV4 brachydanio
28	68	76.4	86	2 Q28241	Q28241 cervus elap
29	68	76.4	112	1 TGFI_BOVIN	P21214 bos taurus
30	68	76.4	224	2 Q8CDZ9	Q8CDZ9 mus musculu
31	68	76.4	255	2 Q921T1	Q921T1 mus musculu

32	68	76.4	399	2 Q9ERB7	Q9ERB7 mesocricetu
33	68	76.4	412	1 TGFI_CHICK	P30371 gallus gall
34	68	76.4	413	1 TGFI_XENIA	P17247 xenopus lae
35	68	76.4	414	1 TGFI_CERAE	P61811 cercopithec
36	68	76.4	414	1 TGFI_HUMAN	P61812 homo sapien
37	68	76.4	414	1 TGFI_MOUSE	P27090 mus musculu
38	68	76.4	414	2 Q91VF5	Q91VF5 mus musculu
39	68	76.4	435	1 TGFI_PIG	P09858 sus scrofa
40	68	76.4	442	1 TGFI_RAT	Q07257 rattus norv
41	68	76.4	442	2 Q6T7C3	Q6T7C3 oryctolagus
42	62	69.7	62	2 Q90YF3	Q90YF3 pleuronecte
43	62	69.7	62	2 Q90YF9	Q90YF9 oncorhynch
44	62	69.7	62	2 Q90Z08	Q90Z08 anguilla an
45	62	69.7	88	2 Q90ZE7	Q90ZE7 acipenser b

## ALIGNMENTS

RESULT 1  
Q28240 PRELIMINARY; PRT; 50 AA.  
AC Q28240.  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Transforming growth factor beta 1 (TGF-beta 1) (Transforming growth factor B1) (Fragment).  
GN Name=TGFBI; Synonyms=TGF beta-1, TGF-B1;  
OS Cervus elaphus (Red deer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;  
OC Cervinae; Cervus.  
OX NCBI\_Taxid=9860;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Antler;  
RX MEDLINE=98233260; PubMed=9571767;  
RX DOI=10.1002/(SICI)1097-010X(19980501)281:1<36::AID-JE26>3.0.CO;2-D;  
RA Francis S.M., Suttle J.M.;  
RT "Detection of growth factors and proto-oncogene mRNA in the growing tip of red deer (Cervus elaphus) antler using reverse-transcriptase  
RT polymerase chain reaction (RT-PCR).";  
RL J. Exp. Zool. 281:36-42(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Wagener A., Blothner S., Fickel J.;  
RT "Detection of growth factors in the testes of roe deer (Capreolus capreolus).";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DERIVATIVES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.  
CC -!- SUBUNIT: Homodimer; disulfide-linked (by similarity).  
CC -!- SIMILARITY: Belongs to the TGF-beta family.  
DR EMBL; U62110; AAB05256.1; -.  
DR EMBL; AF152591; AAF73230.1; -.  
DR HSSP; P01137; IKLA.  
DR GO; GO:0008083; F:growth factor activity; IEA.  
DR GO; GO:0008283; P:cell proliferation; IEA.  
DR GO; GO:0000074; P:regulation of cell cycle; IEA.  
DR InterPro; IPR001839; TGFb.  
DR Pfam; PF00019; TGF\_beta.1.  
DR Prodom; PD000357; TGFb.1.  
DR SMART; SM00204; TGFb.1.  
DR PROSITE; PS00250; TGF\_BETA\_1, 1.  
KW Glycoprotein; Growth factor; Mitogen.  
FT NON TER 1  
FT CHAIN 1  
FT TRANSFORMING GROWTH FACTOR BETA 1.

FT	NON TER	50	50	
SO	SEQUENCE	50 AA;	6012 MW;	0DDDAE46C640759F CRC64;
Query Match				
	Best Local Similarity	100.0%;	Score 89;	DB 2; Length 50;
	Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;
QY	1 FCLGPCPYIWSLDT 14			
Db	35 FCLGPCPYIWSLDT 48			
RESULT 2				
ID	Q72487	PRELIMINARY;	PRT;	51 AA.
AC	Q72487;			
DT	01-OCT-2003 (TREMBLrel. 25, Created)			
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Transforming growth factor beta 1 (Fragment).			
GN	Name=TGFBI;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Vieira A.R., Murray J.C.;			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
CC	-I- SIMILARITY: Belongs to the TGF-beta family.			
DR	EMBL; AY330202; AAQ18642.1; --.			
DR	HSSP; P01137; IKLA.			
DR	GO; GO:0008083; F:growth factor activity; IBA.			
DR	InterPro; IPR001839; TGFb.			
DR	Pfam; PF00019; TGF beta; 1.			
DR	ProDom; PD000357; TGFb; 1.			
DR	SMART; SM00204; TGFBI. 1.			
DR	PROSITE; PS00250; TGF_BETA_1; 1.			
KW	Growth factor.			
FT	NON TER	1		
FT	NON TER	51		
SO	SEQUENCE	51 AA;	6140 MW;	259F4DB23E4A9D0 CRC64;
Query Match				
	Best Local Similarity	100.0%;	Score 89;	DB 2; Length 51;
	Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;
QY	1 FCLGPCPYIWSLDT 14			
Db	34 FCLGPCPYIWSLDT 47			
RESULT 3				
ID	Q70316	PRELIMINARY;	PRT;	78 AA.
AC	Q70316;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Transforming growth factor beta 1 (Fragment).			
GN	Name=TGFBI;			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_Taxid=96023;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kopecky M., Stratil A., Van Poucke M., Bartschlagel H.,			
RL	Geldermann H., Peelman L.J.;			
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.			
CC	-I- SIMILARITY: Belongs to the TGF-beta family.			
DR	EMBL; AJ621785; CAF21862.1; --.			
DR	HSSP; P01137; IKLA.			

DR	GO: GO:0008083; F.growth factor activity; IEA.	
DR	InterPro: IPR001839; TGFb.	
DR	Pfam: PF00019; TGF_beta; 1.	
DR	ProDom: PD000357; TGFb; 1.	
DR	SMART: SM00204; TGFb; 1.	
DR	PROSITE: PS00250; TGF_BETA_1; 1.	
KW	Growth factor.	
FT	NON_TER 1 1	
FT	CHAIN <1 >78 transforming factor beta 1.	
FT	NON_TER 78 78	
SQ	SEQUENCE 78 AA; 8981 MW; IBA179BI47738152 CRC64;	
Query Match 100.0%; Score 89; DB 2; Length 78;		
Best Local Similarity 100.0%; Pred. NO. 2.5e-06;		
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps		
OY	1 FC LGPCPYIWSLDT 14       	
Dd	27 FC LGPCPYIWSLDT 40	
RESULT 4		
ID	002730 PRELIMINARY; PRT; 112 AA.	
AC	002730	
DT	01-JUL-1997 (TrEMBLrel. 04, Created)	
DT	01-JUL-1997 (TrEMBLrel. 04, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Transforming growth factor beta 1 (TGF-beta 1) (Fragment).	
OS	Name=TGFB1; Synonyms=TGF-beta-1; Oryctolagus cuniculus (Rabbit);	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	
OX	NCBI_TaxID=9986;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Taylor T.K., James E.R., McGonigle S., Yoho E.R.;	
RL	Submitted (APR-1997) to the EMBL/Genbank/DDBJ databases.	
RN	[2]	
RA	SEQUENCE OF 2-99 FROM N.A.	
RB	Inoue K., Kawabe Y., Kodama T.;	
RL	Submitted (NOV-1998) to the EMBL/Genbank/DDBJ databases.	
CC	-1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.	
CC	-1- SUBUNIT: Homodimer; disulfide-linked (by similarity).	
CC	-1- SIMILARITY: belongs to the TGF-beta family.	
DR	EMBL; AF000133; AAB53806.1; -.	
DR	HSSP; P01137; IKLA.	
DR	GO: GO:0008083; F.growth factor activity; IEA.	
DR	GO: GO:0008283; P.cell proliferation; IEA.	
DR	GO: GO:0000074; P.regulation of cell cycle; IEA.	
DR	InterPro: IPR002400; GP_cyknob.	
DR	InterPro: IPR001839; TGFb.	
DR	Pfam: PF00019; TGF_beta; 1.	
DR	PRINTS: PR00438; GFCSKNOT.	
DR	ProDom: PD000357; TGFb; 1.	
DR	SMART; SM00204; TGFb; 1.	
DR	PROSITE; PS00250; TGF_BETA_1; 1.	
KW	glycoprotein; Growth Factor; Mitogen.	
FT	NON_TER 1 1	
FT	CHAIN 1 112 TRANSFORMING GROWTH FACTOR BETA 1.	
FT	DISULFID 7 16 BY SIMILARITY.	
FT	DISULFID 15 78 BY SIMILARITY.	
FT	DISULFID 44 109 BY SIMILARITY.	
FT	DISULFID 48 111 BY SIMILARITY.	
FT	DISULFID 77 77 INTERCHAIN (BY SIMILARITY).	
FT	CONFLICT 2 3 ID -> RS (IN REF. 2).	
FT	CONFLICT 85 92 PLPIYIV -> AVAHVVTL (IN REF. 2).	

SQ SEQUENCE 112 AA; 12795 MW; 53CSBYD46355A6F3 CRC64;  
 Query Match 100.0%; Score 89; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYWMSLDT 14  
 |||||  
 Db 43 FCLGPCPYWMSLDT 56

RESULT 5  
 Q95N80 PRELIMINARY; PRT; 124 AA.  
 AC Q95N80;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE Transforming growth factor beta 1 (Fragment)  
 OS Canis familiaris (Dog)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Fontana S., Groene A., Baumgaertner W.;  
 RL Submitted (FE8-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.  
 DR EMBL; AF349538; AAK54072.1; -.  
 DR HSSP; P01137; 1KLA.  
 DR GO; GO:0008083; F: growth factor activity; IEA.  
 DR InterPro; IPR001839; TGFb.  
 DR Pfam; PF000357; TGFb; 1.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Growth factor.  
 FT NON TER 1 1  
 FT NON TER 124 124  
 SQ SEQUENCE 124 AA; 14329 MW; 21D18521B85556DB CRC64;

Query Match 100.0%; Score 89; DB 2; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYWMSLDT 14  
 |||||  
 Db 58 FCLGPCPYWMSLDT 71

RESULT 6  
 Q08714 PRELIMINARY; PRT; 130 AA.  
 ID Q08714; Q70331;  
 AC Q08714; Q70331;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment)  
 GN Name=TGFb1;  
 OS Mesocricetus auratus (Golden hamster)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus  
 NCBI\_TaxID=10036;  
 CX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LVG (SYR);  
 RX MEDLINE=93304479; PubMed=8317544;  
 RA Wong D.T., Donoff R.B., Yang J., Song B.Z., Matrossian K., Nagura N.,  
 RA Elvovic A., McBride J., Gallagher G., Todd R.;  
 RT "Sequential expression of transforming growth factor alpha and beta 1  
 RT by eosinophils during cutaneous wound healing in the hamster.";  
 RL Am. J. Pathol. 143:130-142(1993).

RN [2]  
 RP SEQUENCE OF 26-115 FROM N.A.  
 RC STRAIN=SYRIAN; TISSUE=SPLEEN;  
 RX MEDLINE=98234044; PubMed=9573100;  
 RA Weibly P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;  
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and  
 RT analysis of cytokine mRNA expression in experimental visceral  
 RT leishmaniasis";  
 RL Infect. Immun. 66:2135-2142(1998).

-1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS  
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL  
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF  
 CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1  
 CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND  
 CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.  
 CC -1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED.  
 CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.  
 DR EMBL; X60296; CAA42838.1; -.  
 DR EMBL; AF046214; AAC40099.1; -.  
 DR PIR; I48196; I48196.  
 DR HSSP; P01137; 1KLA.  
 DR GO; GO:0008083; F: growth factor activity; IEA.  
 DR GO; GO:0008283; P: cell proliferation; IEA.  
 DR GO; GO:000074; P: regulation of cell cycle; IEA.  
 DR InterPro; IPR001839; TGFb.  
 DR Pfam; PF000357; TGFb; 1.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Glycoprotein; Growth factor; Mitogen.  
 FT NON TER 1 1  
 FT PRODEP <1 18  
 FT CHAIN 19 130  
 FT DISULFID 25 34  
 FT DISULFID 33 96  
 FT DISULFID 66 129  
 FT DISULFID 95 95  
 FT CONFLICT 93 93  
 SQ SEQUENCE 130 AA; 14997 MW; 8B41DD6C39C9CA77 CRC64;

Query Match 100.0%; Score 89; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 4e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FCLGPCPYWMSLDT 14  
 |||||  
 Db 61 FCLGPCPYWMSLDT 74

RESULT 7  
 TGFL\_BOVIN STANDARD; PRT; 315 AA.  
 ID TGFL\_BOVIN  
 AC P18341;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DE Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment)  
 GN Name=TGFb1;  
 OS Bos taurus (Bovine)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 CX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91042552; PubMed=3153459;  
 RA van Obberghen-Schilling R., Kondiah P., Ludwig R.L., Sporn M.B.,  
 RA Baker C.C.;  
 RT "Complementary deoxyribonucleic acid cloning of bovine transforming  
 RT growth factor-beta 1.";  
 RL Mol. Endocrinol. 1:693-698(1987).  
 RN [2]  
 RP SUBUNITS.

RC TISSUE=Bone; PubMed=1733936;  
 RA MEDLINE=92129307; Daesch J.R., Chang R.J., Glaser C.B.;  
 RT "Purification and characterization of transforming growth factor-beta  
 2.3 and -beta 1.2 heterodimers from bovine bone.";  
 RL J. Biol. Chem. 267:2325-2328 (1992).  
 CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control  
 proliferation, differentiation, and other functions in many cell  
 types. Many cells synthesize TGF-beta and essentially all of them  
 have specific receptors for this peptide. TGF-beta regulates the  
 actions of many other peptide growth factors and determines a  
 positive or negative direction of their effects. Play an important  
 role in bone remodeling. It is a potent stimulator of  
 osteoblastic bone formation, causing chemotaxis, proliferation and  
 differentiation in committed osteoblasts (By similarity).  
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
 covalently linked to a latency-associated peptide (LAP) homodimer.  
 The inactive complex can contain a latent TGF-beta binding protein  
 (By similarity). The active form is a homodimer of mature TGF-beta  
 1; disulfide-linked. Heterodimers of TGF-beta 1/2 have been found  
 in bone.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PFM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
 and LAP (By similarity).  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M36371; AAA30778.1; -.  
 DR PIR; A40057; A40057.  
 DR HSSP; P01137; IKLA.  
 DR InterPro; IPR002400; GF\_cysknoc.  
 DR InterPro; IPR003911; TGF\_TGFB.  
 DR InterPro; IPR001839; TGFB.  
 DR InterPro; IPR001111; TGFB\_N.  
 DR Pfam; PF00019; TGF\_beta\_1.  
 DR PRINTS; PR00688; TGFB\_propeptide; 1.  
 DR PRINTS; PR00438; GFCSKNOT.  
 DR PRINTS; PR01423; TGFBETA.  
 DR ProDom; PD000357; TGFB; 1.  
 DR SMART; SM00204; TGFB; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 DR Glycoprotein; Growth Factor; Mitogen.  
 KW NON\_TER  
 FT PROPEP 1 203  
 FT CHAIN 204 315 Transforming growth factor beta 1.  
 FT DISULFID 210 219 By similarity.  
 FT DISULFID 218 281 By similarity.  
 FT DISULFID 247 312 By similarity.  
 FT DISULFID 251 314 By similarity.  
 FT DISULFID 280 280 Interchain (By similarity).  
 FT CARBOHYD 7 7 N-linked (GlcNAc...) (By similarity).  
 FT CARBOHYD 61 61 N-linked (GlcNAc...) (By similarity).  
 FT CARBOHYD 101 101 N-linked (GlcNAc...) (By similarity).  
 FT SITE 169 171 Cell attachment site (Potential).  
 SQ SEQUENCE 315 AA; 36269 MW; C2717A23D994E00E CRC64;  
 Query Match 100.0%; Score 89; DB 1; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-06; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0;  
 QY 1 FCLGPCPYIWSLDT 14  
 DB 246 FCLGPCPYIWSLDT 259

Q8R4D9  
 ID Q8R4D9 PRELIMINARY; PRT; 368 AA.  
 AC Q8R4D9  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Transforming growth factor beta-1 protein (Fragment).  
 GN Name=Tgfb1;  
 OS Simodon hispidus (Hispid cotton rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 CC Sigmodon.  
 OX NCBI\_TaxID=42415;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14980081; DOI=10.1089/1079900477219873;  
 RA Blanco J.C., Placencia L., Boukhvalova M., Richardson J.Y.,  
 Harris K.A., Prince G.A.;  
 RT "The cotton rat: an underutilized animal model for human infectious  
 diseases can now be exploited using specific reagents to cytokines,  
 chemokines, and interferons.";  
 RT J. Interferon Cytokine Res. 24:21-28 (2004).  
 RL -1- SIMILARITY: Belongs to the TGF-beta family.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PFM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
 and LAP (By similarity).  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.  
 CC -----  
 DR EMBL; AF480858; AA87199.1; -.  
 DR HSSP; P01137; IKLA.  
 DR GO; GO:0008083; F:growth factor activity; IEA.  
 DR GO; GO:0005160; F:transforming growth factor beta receptor bi.; IEA.  
 DR GO; GO:0016049; F:cell growth; IEA.  
 DR InterPro; IPR002400; GF\_cysknoc.  
 DR InterPro; IPR001839; TGFB.  
 DR InterPro; IPR001839; TGFB.  
 DR InterPro; IPR003911; TGF\_TGFB.  
 DR InterPro; IPR001111; TGFB\_N.  
 DR InterPro; IPR00688; TGF\_propeptide; 1.  
 DR Pfam; PF00019; TGF\_beta\_1.  
 DR PRINTS; PR00438; GFCSKNOT.  
 DR PRINTS; PR01423; TGFBETA.  
 DR PRINTS; PR01424; TGFBETA.  
 DR ProDom; PD000357; TGFB; 1.  
 DR SMART; SM00204; TGFB; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Growth factor.  
 FT NON\_TER 1  
 FT SEQUENCE 368 AA; 41905 MW; A5C91207B0468B4A CRC64;  
 Query Match 100.0%; Score 89; DB 2; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FCLGPCPYIWSLDT 14  
 DB 299 FCLGPCPYIWSLDT 312  
 RESULT 9  
 ID TGF1\_CANFA STANDARD; PRT; 390 AA.  
 AC P54831;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
 GN Name=Tgfb1;  
 OS Canis familiaris (Dog).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Jugular vein endothelial;  
 RX MEDLINE=95237630; PubMed=7721110; DOI=10.1016/0378-1119(94)00903-6;  
 RA Manning A.W., Auchampach J.A., Drong R.F., Slightom J.L.;  
 RT "Cloning of a canine CDNA homologous to the human transforming growth

RT factor-beta 1-encoding gene.";  
 RL Gene 155:307-308(1995).  
 CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control  
 CC proliferation, differentiation, and other functions in many cell  
 CC types. Many cells synthesize TGF-beta and essentially all of them  
 CC have specific receptors for this peptide. TGF-beta regulates the  
 CC actions of many other peptide growth factors and determines a  
 CC positive or negative direction of their effects. Play an important  
 CC role in bone remodeling. It is a potent stimulator of  
 CC osteoblastic bone formation, causing chemotaxis, proliferation and  
 CC differentiation in committed osteoblasts (By similarity).  
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
 CC covalently linked to a latency-associated peptide (LAP) homodimer.  
 CC The inactive complex can contain a latent TGF-beta binding  
 CC protein. The active form is a homodimer of mature TGF-beta 1;  
 CC disulfide-linked (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
 CC and LAP (By similarity).  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.  
 CC -----  
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 CC -----  
 DR EMBL: L34956; AAA51458.1; -.  
 DR PIR: J04023; J04023.  
 DR HSSP: P01137; IKLA.  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR003911; TGF\_TGFB.  
 DR InterPro: IPR01839; TGFb.  
 DR InterPro: IPR01111; TGFb\_N.  
 DR Pfam: PF00019; TGF\_beta; 1.  
 DR Pfam: PF00688; TGFb\_propeptide; 1.  
 DR PRINTS: PR00438; GRCYSKNOT.  
 DR PRINTS: PR01423; TGRBETA.  
 DR PRODOM: PD000357; TGFb; 1.  
 DR SMART: SM00204; TGFb; 1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 KM Glycoprotein; Growth Factor; Mitogen; Signal.  
 FT STGNL 1 29  
 FT PROPEP 30 28  
 FT FT 279 390  
 FT CHAIN 285 294  
 FT DISULFID 293 356  
 FT DISULFID 322 387  
 FT DISULFID 326 389  
 FT DISULFID 355 355  
 FT CARBOHYD 82 82  
 FT CARBOHYD 136 136  
 FT CARBOHYD 176 176  
 FT SITE 244 246  
 SQ SEQUENCE 390 AA; 44185 MW; E84780E88B7B590E CRC64;  
 Query Match 100.0%; Score 89; DB 1; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 1;le-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DT 05-JUL-2004 (Rel. 44, last annotation update)  
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
 GN Name=TGFb1;  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OK NCBI\_TaxId=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Hartley;  
 RA Jeevan A., McMurray D.N., Yoshimura T.;  
 RT "Guinea pig transforming growth factor-beta in peritoneal exudates  
 RT after BCG vaccination.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 265-382 FROM N.A.  
 RX MEDLINE=99144670; PubMed=10025978; DOI=10.1016/S1043-4666(98)90002-3;  
 RA Scarozza A.M., Ramsingh A.I., Wicher V., Wicher K.;  
 RT "Spontaneous cytokine gene expression in normal guinea pig blood and  
 RT tissues".  
 RL Cytokine 10:851-859(1998).  
 RN [3]  
 RP SEQUENCE OF 279-371 FROM N.A.  
 RC STRAIN=Hartley; TISSUE=Trachea;  
 RA Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,  
 RA Seizawa K.;  
 RT "Guinea-pig transforming growth factor-beta expression in injured  
 RT tracheal epithelium.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Multifunctional peptide that controls proliferation,  
 CC differentiation, and other functions in many cell types. Many  
 CC cells synthesize TGF-beta 1 and essentially all of them have  
 CC specific receptors for this peptide. TGF-beta 1 regulates the  
 CC actions of many other peptide growth factors and determines a  
 CC positive or negative direction of their effects. Play an important  
 CC role in bone remodeling. It is a potent stimulator of  
 CC osteoblastic bone formation, causing chemotaxis, proliferation and  
 CC differentiation in committed osteoblasts (By similarity).  
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
 CC covalently linked to a latency-associated peptide (LAP) homodimer.  
 CC The inactive complex can contain a latent TGF-beta binding  
 CC protein. The active form is a homodimer of mature TGF-beta 1;  
 CC disulfide-linked (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
 CC and LAP (By similarity).  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.  
 CC -----  
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 CC -----  
 DR EMBL: AF191297; AF02780.1; -.  
 DR EMBL: AF097509; AAC83807.1; -.  
 DR EMBL: AF169347; AAD49347.1; -.  
 DR HSSP: P01137; IKLA.  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR003911; TGF\_TGFB.  
 DR InterPro: IPR001839; TGFb.  
 DR InterPro: IPR01111; TGFb\_N.  
 DR Pfam: PF00019; TGF\_beta; 1.  
 DR Pfam: PF00688; TGFb\_propeptide; 1.  
 DR PRINTS: PR00438; GRCYSKNOT.  
 DR PRINTS: PR01423; TGRBETA.  
 DR PRODOM: PD000357; TGFb; 1.  
 DR SMART: SM00204; TGFb; 1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 KM Glycoprotein; Growth Factor; Mitogen; Signal.

FT SIGNAL 1 29 By similarity.  
 FT PROPER 30 278 latency-associated peptide (By  
 FT CHAIN 279 390 similarity).  
 FT DISULFID 285 294 Transforming growth factor beta 1.  
 FT DISULFID 293 356 By similarity.  
 FT DISULFID 322 387 By similarity.  
 FT DISULFID 326 389 By similarity.  
 FT DISULFID 355 355 Interchain (By similarity).  
 FT CARBOHYD 82 82 N-linked (GlcNAc...) (By similarity).  
 FT CARBOHYD 136 136 N-linked (GlcNAc...) (By similarity).  
 FT CARBOHYD 176 176 Cell attachment site (Potential).  
 FT SITE 244 246 G->P (in Ref. 3).  
 FT CONFLICT 279 279 F->S (in Ref. 2).  
 FT CONFLICT 286 286 K->E (in Ref. 2).  
 FT CONFLICT 309 309 C->R (in Ref. 2).  
 FT CONFLICT 322 322 A->G (in Ref. 2).  
 FT CONFLICT 350 350  
 FT SEQUENCE 390 AA; 44328 MW; 1539F849BA0C0CF1 CRC64;

Query Match Best Local Similarity 100.0%; Score 89; DB 1; Length 390;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCIGPCPYIWSLDT 14  
 Db 321 FCIGPCPYIWSLDT 334

RESULT 11  
 TGF1\_CERAE STANDARD; PRT; 390 AA.  
 ID\_TGF1\_CERAE  
 AC P09533;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
 GN Name=TGFb1;  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OC NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=67246074; PubMed=3474130;  
 RA Sharples K., Plowman G.D., Rose T.M., Twardzik D.R., Purchio A.F.;  
 RT "Cloning and sequence analysis of simian transforming growth factor-  
 beta cDNA.";  
 RL DNA 6:239-244(1987).  
 RL [2]  
 RN  
 RP GLYCOSYLATION.  
 RX PubMed=2971654;  
 RA Purchio A.F., Cooper J.A., Brunner A.M., Lioubin M.N., Gentry L.E.,  
 RA Kovachina K.S., Roth R.A., Marguardt H.;  
 RT "Identification of mannose 6-phosphate in two asparagine-linked sugar  
 chains of recombinant transforming growth factor-beta 1 precursor.";  
 RL J. Biol. Chem. 263:14211-14215(1988).  
 RN [3]  
 RN CHARACTERIZATION.

RA Gentry L.E., Lioubin M.N., Purchio A.F., Marguardt H.;  
 RT "Molecular events in the processing of recombinant type 1 pre-pro-  
 transforming growth factor beta to the mature polypeptide.";  
 RL Mol. Cell. Biol. 8:4162-4168(1988).  
 CC -1- FUNCTION: Multifunctional peptide that controls proliferation,  
 differentiation, and other functions in many cell types. Many  
 cells synthesize TGF-beta 1 and essentially all of them have  
 specific receptors for this peptide. TGF-beta 1 regulates the  
 actions of many other peptide growth factors and determines a  
 positive or negative direction of their effects. Play an important  
 role in bone remodelling. It is a potent stimulator of  
 osteoblastic bone formation, causing chemotaxis, proliferation and

CC differentiation in committed osteoblasts (By similarity).  
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
 covalently linked to a latency-associated peptide (LAP) homodimer.  
 CC The inactive complex can contain a latent TGF-beta binding  
 CC protein. The active form is a homodimer of mature TGF-beta 1;  
 CC disulfide-linked.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC and LAP, which remains non-covalently linked to mature TGF-beta 1  
 CC rendering it inactive.  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.

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DR EMBL; M16658; AAA35369.1; -.  
 DR PIR; A26960; A26960.  
 DR HSSP; P01137; IRLA.  
 DR InterPro; IPR002400; GF\_cysknot.  
 DR InterPro; IPR003911; TGF\_TGFB.  
 DR InterPro; IPR001839; TGFB.  
 DR InterPro; IPR001111; TGFB\_N.  
 DR Pfam; PF00019; TGF\_beta; 1.  
 DR Pfam; PF00688; TGFB\_propeptide; 1.  
 DR PRINTS; PRO0438; GRCYSKNOT.  
 DR PRINTS; PRO1423; TGFBETA.  
 DR PRODOM; PD000357; TGFB; 1.  
 DR SMART; SM00204; TGFB; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 DR GlycoProtein; Growth Factor; Mitogen; Signal.

FT SIGNAL 1 29  
 FT PROPER 30 278 latency-associated peptide.  
 FT CHAIN 279 390 Transforming growth factor beta 1.  
 FT DISULFID 285 294 By similarity.  
 FT DISULFID 293 356 By similarity.  
 FT DISULFID 322 387 By similarity.  
 FT DISULFID 326 389 By similarity.  
 FT DISULFID 355 355 Interchain (By similarity).  
 FT CARBOHYD 82 82 N-linked (GlcNAc...) (By similarity).  
 FT CARBOHYD 136 136 N-linked (GlcNAc...) (By similarity).  
 FT CARBOHYD 176 176 Cell attachment site (Potential).  
 FT SITE 244 246  
 FT SEQUENCE 390 AA; 44356 MW; DFF63E2BAB46320B CRC64;

Query Match Best Local Similarity 100.0%; Score 89; DB 1; Length 390;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FCIGPCPYIWSLDT 14  
 Db 321 FCIGPCPYIWSLDT 334

RESULT 12  
 TGF1\_HORSE STANDARD; PRT; 390 AA.  
 ID\_TGF1\_HORSE  
 AC O19011;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
 GN Name=TGFb1;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OC NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Gentry L.E., Lioubin M.N., Purchio A.F., Marguardt H.;  
 RT "Molecular events in the processing of recombinant type 1 pre-pro-  
 transforming growth factor beta to the mature polypeptide.";  
 RL Mol. Cell. Biol. 8:4162-4168(1988).  
 CC -1- FUNCTION: Multifunctional peptide that controls proliferation,  
 differentiation, and other functions in many cell types. Many  
 cells synthesize TGF-beta 1 and essentially all of them have  
 specific receptors for this peptide. TGF-beta 1 regulates the  
 actions of many other peptide growth factors and determines a  
 positive or negative direction of their effects. Play an important  
 role in bone remodelling. It is a potent stimulator of  
 osteoblastic bone formation, causing chemotaxis, proliferation and

CC TISSUE=Lymph node;  
 RX MEDLINE=98185507; PubMed=9524819;  
 RA Penha-Goncalves M.N., Onions D.E., Nicolson L.;  
 RT "Cloning and sequencing of equine transforming growth factor-beta 1  
 (TGF-beta-1) cDNA.";  
 RL DNA Seq. 7:375-378(1997).  
 CC -1 FUNCTION: TGF-beta is a multifunctional peptide that control  
 proliferation, differentiation, and other functions in many cell  
 types. Many cells synthesize TGF-beta and essentially all of them  
 have specific receptors for this peptide. TGF-beta regulates the  
 actions of many other peptide growth factors and determines  
 positive or negative direction of their effects. Play an important  
 role in bone remodelling. It is a potent stimulator of  
 osteoblastic bone formation, causing chemotaxis, proliferation and  
 differentiation in committed osteoblasts (by similarity).  
 CC -1 SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
 covalently linked to a latency-associated peptide (LAP) homodimer.  
 CC The inactive complex can contain a latent TGF-beta binding  
 protein. The active form is a homodimer of mature TGF-beta 1;  
 CC disulfide-linked (by similarity).  
 CC -1 SUBCELLULAR LOCATION: Secreted.  
 CC -1 PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
 and LAP (by similarity).  
 CC -1 SIMILARITY: Belongs to the TGF-beta family.  
 CC -----  
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 or send an email to [license@sib.ch](mailto:license@sib.ch)).  
 CC -----  
 DR EMBL; X99438; CAA67801.1; -;  
 DR HSPB; P01137; 1KLA.  
 DR InterPro: IPR002400; GF\_cysknob.  
 DR InterPro: IPR003911; TGF\_TGFB.  
 DR InterPro: IPR001839; TGFb.  
 DR InterPro: IPR001111; TGFb\_N.  
 DR Pfam; PF00019; TGF\_beta\_1.  
 DR Pfam; PF00688; TGFb\_propeptide\_1.  
 DR PRINTS; PR00438; GFCYSKNOT.  
 DR PRINTS; PR01423; TGFbeta.  
 DR PRODOM; PD000357; TGFb\_1.  
 DR SMART; SM00204; TGFb\_1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KM Glycoprotein; Growth factor; Mitogen; Signal.  
 FT SIGNAL 1 29  
 FT PROPEP 30 278  
 FT CHAIN 279 390  
 FT DISULFID 285 294  
 FT DISULFID 293 356  
 FT DISULFID 322 387  
 FT DISULFID 326 389  
 FT DISULFID 355 355  
 FT CARBOHYD 82 82  
 FT CARBOHYD 136 136  
 FT CARBOHYD 176 176  
 SQ SEQUENCE 390 AA; 43974 MW; A86D715F44549691 CRC64;  
 Query Match 100.0%; Score 89; DB 1; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 1.le-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC P01137; Q9UCG4;  
 DT 21-JUN-1986 (Rel. 01, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
 GN Name=TGFb1; Synonyms=TGFb;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OK NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87174845; PubMed=3470709;  
 RA Derynck R., Rhee L., Chen E.Y., van Tilburg A.;  
 RT "Intron-exon structure of the human transforming growth factor-beta  
 precursor gene.";  
 RL Nucleic Acids Res. 15:3188-3189(1987).  
 RN (2)  
 RP SEQUENCE FROM N.A., AND VARIANT PRO-10.  
 RX MEDLINE=85296301; PubMed=3861940;  
 RA Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,  
 RA Assoian R.K., Roberts A.B., Sporn M.B., Goeddel D.V.;  
 RT "Human transforming growth factor-beta complementary DNA sequence and  
 expression in normal and transformed cells.";  
 RL Nature 316:701-705(1985).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Dundenum, and Eye;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Aleschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C.,  
 RA Rahn S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halyk S.W.,  
 RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska V., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL (4)  
 RP SEQUENCE OF 279-390 FROM N.A.  
 RC TISSUE=Cardioma;  
 RA Urushizaki Y., Tereu T., Koshida Y., Mahara K., Kohgo Y.,  
 RA Urushizaki I., Takahashi Y., Ito H.;  
 RT "Cloning and expression of the gene for human transforming growth  
 factor-beta in *Escherichia coli*.";  
 RL Tumor Res. 22:41-55(1987).  
 RN (5)  
 RP SEQUENCE OF 279-329.  
 RC TISSUE=Bladder carcinoma;  
 RX MEDLINE=93229900; PubMed=8471846; DOI=10.1006/prep.1993.1019;  
 RA Bourdrel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugerman B.J.,  
 RA Hu S., Westcott K.R.;  
 RT "Recombinant human transforming growth factor-beta 1: expression by  
 Chinese hamster ovary cells, isolation, and characterization.";  
 RL Protein Expr. Purif. 4:130-140(1993).  
 RN (6)  
 RP SEQUENCE OF 279-301.  
 RX MEDLINE=85131019; PubMed=2982829;  
 RA Massague J., Like B.;  
 RT "Cellular receptors for type beta transforming growth factor. Ligand  
 binding and affinity labeling in human and rodent cell lines.";  
 RL J. Biol. Chem. 260:2636-2645(1985).

[7]  
 RP SEQUENCE OF 30-42 AND 279-290. AND CHARACTERIZATION.  
 RX PubMed=3162913;  
 RA Miyazono K., Hellman U., Wernstedt C., Heldin C.H.;  
 RT "Latent high molecular weight complex of transforming growth factor  
 beta 1. Purification from human platelets and structural  
 characterization.";  
 RL J. Biol. Chem. 263:6407-6415 (1988).  
 RN [8]  
 RP REVIEW.  
 RX PubMed=9150447;  
 RA Munger J.S., Hapel J.G., Gleizes P.E., Mazzieri R., Nunes I.,  
 RA Rifkin D.B.;  
 RT "Latent transforming growth factor-beta: structural features and  
 mechanisms of activation.";  
 RL Kidney Int. 51:1376-1382 (1997).  
 RN [9]  
 RP STRUCTURE BY NMR OF 279-390.  
 RX MEDLINE=93144313; PubMed=8424942;  
 RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,  
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,  
 RA Torchia D.A.;  
 RT "Transforming growth factor beta 1: NMR signal assignments of the  
 recombinant protein expressed and isotopically enriched using Chinese  
 hamster ovary cells.";  
 RL Biochemistry 32:1152-1163 (1993).  
 RN [10]  
 RP STRUCTURE BY NMR OF 279-390.  
 RX MEDLINE=93144320; PubMed=8424943;  
 RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,  
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,  
 RA Torchia D.A.;  
 RT "Transforming growth factor beta 1: secondary structure as determined  
 by heteronuclear magnetic resonance spectroscopy.";  
 RL Biochemistry 32:1164-1171 (1993).  
 RN [11]  
 RP STRUCTURE BY NMR OF 279-390.  
 RX MEDLINE=96266150; PubMed=8679613; DOI=10.1021/bi9604946;  
 RA Hinck A.P., Archer S.J., Qian S.W., Roberts A.B., Sporn M.B.,  
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,  
 RA Torchia D.A.;  
 RT "Transforming growth factor beta 1: three-dimensional structure in  
 solution and comparison with the X-ray structure of transforming  
 growth factor beta 2.";  
 RL Biochemistry 35:8517-8534 (1996).  
 RN [12]  
 RP TISSUE SPECIFICITY.  
 RX PubMed=11746498; DOI=10.1002/jcb.1249;  
 RA Shur I., Lokietz F., Bleiberg I., Benayahu D.;  
 RT "Differential gene expression of cultured human osteoblasts.";  
 RL J. Cell. Biochem. 83:547-553 (2001).  
 RN [13]  
 RP VARIANT PRO-10.  
 RX PubMed=9783545;  
 RA Yamada Y., Miyauchi A., Goto J., Takagi Y., Okizumi H., Kanematsu M.,  
 RA Hase M., Takai H., Harada A., Ikeda K.;  
 RT "Association of a polymorphism of the transforming growth factor-beta1  
 gene with genetic susceptibility to osteoporosis in postmenopausal  
 Japanese women.";  
 RL J. Bone Miner. Res. 13:1569-1576 (1998).  
 RN [14]  
 RP VARIANTS CED CYS-218, HIS-218 AND ARG-225.  
 RX PubMed=10973241; DOI=10.1038/79128;  
 RA Kinoshita A., Saito T., Tomita H., Makita Y., Yoshida K., Ghadami M.,  
 RA Yamada K., Kondo S., Ikegawa S., Nishimura G., Fukushima Y.,  
 RA Nakagomi T., Saito H., Sugimoto T., Kamegaya M., Hise K., Murray J.C.,  
 RA Taniguchi N., Nishikawa N., Yoshitake K.;  
 RT "Domain-specific mutations in TGFB1 result in Camurati-Engelmann  
 disease.";  
 RL Nat. Genet. 26:19-20 (2000).  
 RN [15]  
 RP VARIANTS CED HIS-81, CYS-218 AND ARG-225.  
 RX PubMed=11062463; DOI=10.1038/81563;

RA Janssens K., Gershoni-Baruch R., Guanabens N., Migone N., Ralston S.,  
 RA Bonduelie M., Lissens W., Van Maldergem L., Vanhoenacker F.,  
 RA Verbruggen L., Van Hul W.;  
 RT "Mutations in the gene encoding the latency-associated peptide of TGF-  
 beta 1 cause Camurati-Engelmann disease.";  
 RL Nat. Genet. 26:273-275 (2000).  
 RN [16]  
 RP VARIANT PRO-10.  
 RX PubMed=12202987; DOI=10.1007/s100380200069;  
 RA Watanabe Y., Kinoshita A., Yamada T., Ohta T., Kishino T.,  
 RA Matsunoto N., Ishikawa M., Nishikawa N., Yoshitake K.;  
 RT "A catalog of 106 single-nucleotide polymorphisms (SNPs) and 11 other  
 types of variations in genes for transforming growth factor-beta1  
 (TGF-beta1) and its signaling pathway.";  
 RL J. Hum. Genet. 47:478-483 (2002).  
 RN [17]  
 RP CHARACTERIZATION OF VARIANTS CED HIS-81, CYS-218, ASP-222 AND ARG-225.  
 RX PubMed=12493741; DOI=10.1074/jbc.M208857200;  
 RA Janssens K., ten Dijke P., Ralston S.H., Bergmann C., Van Hul W.;  
 RT "Transforming growth factor-beta-1 mutations in Camurati-Engelmann  
 disease lead to increased signaling by altering either activation or  
 secretion of the mutant protein.";  
 RL J. Biol. Chem. 278:7718-7724 (2003).  
 RN [18]  
 RP CHARACTERIZATION OF VARIANT CYS-218.  
 RX PubMed=12843182; DOI=10.1210/jc.2002-020564;  
 RA McGowan N.W., Macpherson H., Janssens K., Van Hul W., Fitch J.C.,  
 RA Fraser W.D., Ralston S.H., Helfrich M.H.;  
 RT "A mutation affecting the latency-associated peptide of TGFbeta1 in  
 Camurati-Engelmann disease enhances osteoclast formation in vitro.";  
 RL J. Clin. Endocrinol. Metab. 88:3321-3326 (2003).  
 CC -1 FUNCTION: Multifunctional peptide that controls proliferation,  
 CC differentiation, and other functions in many cell types. Many  
 CC cells synthesize TGF-beta 1 and essentially all of them have  
 CC specific receptors for this peptide. TGF-beta 1 regulates the  
 CC actions of many other peptide growth factors and determines a  
 CC positive or negative direction of their effects. Play an important  
 CC role in bone remodeling. It is a potent stimulator of  
 CC osteoblastic bone formation, causing chemotaxis, proliferation and  
 CC differentiation in committed osteoblasts (By similarity).  
 CC -1 SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
 CC covalently linked to a latency-associated peptide (LAP) homodimer.  
 CC The inactive complex can contain a latent TGF-beta binding  
 CC protein. The active form is a homodimer of mature TGF-beta 1;  
 CC disulfide-linked.  
 CC -1 SUBCELLULAR LOCATION: Secreted.  
 CC -1 TISSUE SPECIFICITY: Highly expressed in bone.  
 CC -1 INDUCTION: Activated in vitro at pH below 3.5 and over 12.5.  
 CC -1 PTM: Glycosylated (By similarity). The precursor is cleaved into  
 CC mature TGF-beta 1 and LAP.  
 CC -1 POLYMORPHISM: In post-menopausal Japanese women, the frequency of  
 CC Leu-10 is higher in subjects with osteoporosis than in controls.  
 CC -1 DISEASE: Defects in TGFB1 are the cause of Camurati-Engelmann

Query Match 100.0%; Score 89; DB 1; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 FCLGCPYIWSLDT 14  
 Db 321 FCLGCPYIWSLDT 334

RESULT 14  
 TGFB1 MOUSE  
 ID \_TGFB1 MOUSE STANDARD; PRT; 390 AA.  
 AC P04202;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 20-MAR-1987 (Rel. 04, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
 GN Name=lgfb1;  
 OS Mus musculus (Mouse).



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86168129; PubMed=3007454;  
 RA Derynck R., Jarrett J.A., Chen B.Y., Goeddel D.V.,  
 RT "The murine transforming growth factor-beta precursor.";  
 RL J. Biol. Chem. 261:4377-4379(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BA6/c;  
 RX MEDLINE=96096545; PubMed=8522200; DOI=10.1016/0378-1119(95)00460-N;  
 RA Guron C., Sudarshan C., Raghov R.,  
 RT "Molecular organization of the gene encoding murine transforming  
 RT growth factor beta 1.";  
 RL Gene 165:325-326(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6, and NOD/Lt; TISSUE=Spleen;  
 RA Polrot L., Benoist C., Mathis D.,  
 RT "Transforming growth factor-beta 1 sequence and expression: no  
 RT difference between NOD/Lt and C57BL/6 mouse strains.";  
 RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinot P., Frange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control  
 CC proliferation, differentiation, and other functions in many cell  
 CC types. Many cells synthesize TGF-beta and essentially all of them  
 CC have specific receptors for this peptide. TGF-beta regulates the  
 CC actions of many other peptide growth factors and determines a  
 CC positive or negative direction of their effects. Play an important  
 CC role in bone remodelling. It is a potent stimulator of  
 CC osteoblastic bone formation, causing chemotaxis, proliferation and  
 CC differentiation in committed osteoblasts (by similarity).  
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
 CC covalently linked to a latency-associated peptide (LAP) homodimer.  
 CC The inactive complex can contain a latent TGF-beta binding  
 CC protein. The active form is a homodimer of mature TGF-beta 1;  
 CC disulfide-linked (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
 CC and LAP (by similarity).  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.  
 CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 CC -----  
 CC EMBL; M13177; AAA40423.1; -;  
 CC EMBL; L42462; AAB00138.1; -;  
 CC EMBL; L42456; AAB00138.1; JOINED.  
 CC EMBL; L42457; AAB00138.1; JOINED.  
 CC EMBL; L42458; AAB00138.1; JOINED.  
 CC EMBL; L42459; AAB00138.1; JOINED.  
 CC EMBL; L42460; AAB00138.1; JOINED.  
 CC EMBL; L42461; AAB00138.1; JOINED.  
 CC EMBL; A3009862; CAA08900.1; -;  
 CC EMBL; BC013738; AAH13738.1; -;  
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 CC HSSP; P01137; IKLA.  
 CC MGD; MGI:98725; Tgfb1.  
 CC GO; GO:0005578; C:extracellular matrix; IDA.  
 CC GO; GO:0006954; P:inflammatory response; IMP.  
 CC GO; GO:0007515; P:lymph gland development; IMP.  
 CC GO; GO:0006820; P:necrosis; IMP.  
 CC GO; GO:0006468; P:protein amino acid phosphorylation; IDA.  
 CC GO; GO:0042127; P:regulation of cell proliferation; IDA.  
 CC GO; GO:0042306; P:regulation of protein-nucleus import; IDA.  
 CC GO; GO:0007179; P:transforming growth factor beta receptor si. .; IDA.  
 CC InterPro; IPR002400; GF\_cy8knob.  
 CC InterPro; IPR003911; TGF\_TGFB.  
 CC InterPro; IPR001839; TGF.  
 CC InterPro; IPR001111; TGFb\_N.  
 CC Pfam; PF00019; TGF\_beta; 1.  
 CC Pfam; PF00688; TGFb\_propeptide; 1.  
 CC PRINTS; PR00438; GFCSKNOT.  
 CC PRINTS; PR01423; TGFbeta.  
 CC ProDom; PD000357; TGFb\_1.  
 CC PROSITE; PS00250; TGF\_BETA\_1; 1.  
 CC KAM; Glycoprotein; Growth factor; Mitogen; Signal.  
 CC FT SIGNAL 1 29  
 CC FT PROPEP 30 278  
 CC FT CHAIN 279 390  
 CC FT DISULFD 285 294  
 CC FT DISULFD 293 356  
 CC FT DISULFD 322 387  
 CC FT DISULFD 326 389  
 CC FT DISULFD 355 355  
 CC FT CARBOHYD 82 82  
 CC FT CARBOHYD 136 136  
 CC FT CARBOHYD 176 176  
 CC FT SITE 244 246  
 CC SQ SEQUENCE 390 AA; 44310 MW; 4381A51B711D689E CRC64;  
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 CC Query Match 100.0%; Score 89; DB 1; Length 390;  
 CC Best local Similarity 100.0%; Pred. No. 1.1e-05;  
 CC Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
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 CC DB 321 FCLGPCPYMSLDT 334  
 CC  
 CC RESULT 15  
 CC ID TGF1\_PIG STANDARD; PRT; 390 AA.  
 CC AC P07200; P08832;  
 CC DT 01-APR-1988 (Rel. 07, Created)  
 CC DT 01-APR-1988 (Rel. 07, Last sequence update)  
 CC DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 CC DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
 CC GN Name=TGFb1;  
 CC OS Sus scrofa (Pig).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 CC OX NCBI\_TaxId=9823;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;  
RX MEDLINE=87174844; PubMed=3470708;  
RA Derynck R., Rhee L.;  
RT "Sequence of the porcine transforming growth factor-beta precursor";  
RL Nucleic Acids Res. 15:3187-3187(1987).  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANT VAL-114.  
RC STRAIN=miniature swine;  
RX MEDLINE=89054010; PubMed=2461367;  
RA Kondaliah P., van Obberghen-Schilling E., Ludwig R.L., Dhar R.,  
RA Sporn M.B., Roberts A.B.;  
RT "cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.  
RT Evidence for alternate splicing and polyadenylation.";  
RL J. Biol. Chem. 263:18313-18317(1988).  
RN [3]  
RP SEQUENCE FROM N.A., AND VARIANT VAL-114.  
RX MEDLINE=8835639; PubMed=3166520;  
RA Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;  
RT "Nucleotide sequence of chicken transforming growth factor-beta 1  
RT (TGF-beta 1).";  
RL Nucleic Acids Res. 16:8730-8730(1988).  
RN [4]  
RP SHOWS THAT REF.3 SEQUENCE IS FROM PTG.  
RA Jakowlew S.B.;  
RL Unpublished observations (MAR-1996).  
RN [5]  
RP SEQUENCE FROM N.A., AND VARIANT VAL-114.  
RA Wimmers K., Chomdej S., Ponsuksilli S., Schellander K.;  
RT "Polymorphism in the porcine transforming growth factor beta 1 gene";  
RL Submitted (DBC-2001) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 279-322.  
RX MEDLINE=87102890; PubMed=2879635; DOI=10.1016/0092-8674(87)90192-9;  
RA Chelifetz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E.,  
RA Lucas R., Massague J.;  
RT "The transforming growth factor-beta system, a complex pattern of  
RT cross-reactive ligands and receptors.";  
RL Cell 48:409-415(1987).  
RN [7]  
RP FUNCTION: TGF-beta is a multifunctional peptide that control  
CC proliferation, differentiation, and other functions in many cell  
CC types. Many cells synthesize TGF-beta and essentially all of them  
CC have specific receptors for this peptide. TGF-beta regulates a  
CC positive or negative direction of their effects. Play an important  
CC role in bone remodeling. It is a potent stimulator of  
CC osteoblastic bone formation, causing chemotaxis, proliferation and  
CC differentiation in committed osteoblasts (By similarity).  
CC [8]  
CC SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
CC covalently linked to a latency-associated peptide (LAP) homodimer.  
CC The inactive complex can contain a latent TGF-beta binding  
CC protein. The active form is a homodimer of mature TGF-beta 1;  
CC disulfide-linked (By similarity).  
CC [9]  
CC SUBCELLULAR LOCATION: Secreted.  
CC [10]  
CC PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
CC and LAP (By similarity).  
CC [11]  
CC SIMILARITY: Belongs to the TGF-beta family.  
CC [12]  
CC CAUTION: Ref.3 sequence which was said to originate from chicken  
CC white leghorn, seems (Ref.4) to originate from pig.  
CC [13]  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC [14]  
CC EMBL; Y00111; CA68291.1; -;  
CC EMBL; M23703; AAA64616.1; -;  
CC EMBL; X12373; CAA30933.1; -;  
CC EMBL; AF461808; AAL57902.1; -;  
CC F01; A27512; A27512.  
CC F01; S01413; S01413.

DR HSSP; P01137; IRLA.  
DR InterPro; IPR002400; GF\_cysknot.  
DR InterPro; IPR003911; TGF\_TGFD.  
DR InterPro; IPR001839; TGFb.  
DR InterPro; IPR001111; TGFb\_N.  
DR Pfam; PF00019; TGF\_beta; I.  
DR Pfam; PF00688; TGFb\_propeptide; 1.  
DR PRINTS; PR00438; GFCYSKNOT.  
DR PRINTS; PR01423; TGFbeta.  
DR ProDom; PD000357; TGFb; 1.  
DR SMART; SM00204; TGFb; 1.  
DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
KM Direct protein sequencing; Glycoprotein; Growth factor; Mitogen;  
KM Polymorphism; Signal.  
FT SIGNAL 1 29  
FT PROPEP 30 278 By similarity.  
FT CHAIN 279 390 Transforming growth factor beta 1.  
FT DISULFID 285 294 By similarity.  
FT DISULFID 293 356 By similarity.  
FT DISULFID 322 387 By similarity.  
FT DISULFID 326 389 By similarity.  
FT DISULFID 355 355 Interchain (By similarity).  
FT CARBOHYD 82 82 N-linked (GlcNAc...) (By similarity).  
FT CARBOHYD 136 136 N-linked (GlcNAc...) (By similarity).  
FT CARBOHYD 176 176 N-linked (GlcNAc...) (By similarity).  
FT SITE 244 246 Cell attachment site (Potential).  
FT VARIANT 114 114 L -> V.  
FT CONFLICT 6 7 LR -> PG (In Ref. 3).  
FT CONFLICT 180 180 R -> G (In Ref. 3).  
FT CONFLICT 237 237 N -> NA (In Ref. 3).  
SQ SEQUENCE 390 AA; 44294 MW; A6E2C3659FC384E6 CRC64;

Query Match 100.0%; Score 89; DB 1; Length 390;  
Best Local Similarity 100.0%; Pred. No. 1; e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FCLGPCPYISLDT 14  
DB 321 FCLGPCPYISLDT 334

Search completed: June 14, 2005, 15:51:06  
Job time : 74.8462 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 14, 2005, 15:29:15 ; Search time 131.808 Seconds  
(without alignments)  
67.488 Million cell updates/sec

Title: US-09-831-253f-10

Perfect score: 145

Sequence: 1 HEPKGYANFCLGPGCPYIWSLDT 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database : A: Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	23	3	AA92983 Transform
2	145	100.0	23	3	AA92984 Transform
3	145	100.0	50	2	AA90828 Pre-trans
4	145	100.0	51	2	AA904075 Sequence
5	145	100.0	51	4	AA78788 Human tra
6	145	100.0	51	4	AB843879 Peptide #
7	145	100.0	51	4	AA77799 Peptide #
8	145	100.0	51	4	AA77605 Human bon
9	145	100.0	51	5	AB646640 Human pep
10	145	100.0	62	4	AA68685 Human TGF
11	145	100.0	62	4	AA68685 Human TGF
12	145	100.0	65	2	AA22135 PDGI subu
13	145	100.0	98	2	AA16697 WO9914235
14	145	100.0	98	3	AA92554 TGF-beta
15	145	100.0	98	3	AA92554 TGF-beta
16	145	100.0	98	3	AA92554 TGF-beta
17	145	100.0	112	2	AA808142 Platelet
18	145	100.0	112	2	AA808142 Platelet
19	145	100.0	112	2	AA812402 Transform
20	145	100.0	112	2	AA812402 Transform
21	145	100.0	112	2	AA812402 Transform
22	145	100.0	112	2	AA812402 Transform
23	145	100.0	112	2	AA812402 Transform
24	145	100.0	112	2	AA812402 Transform
25	145	100.0	112	2	AA812402 Transform

26	145	100.0	112	2	AA78781 Human tra
27	145	100.0	112	2	AA97091 The matur
28	145	100.0	112	2	AA90829 Human gro
29	145	100.0	112	2	AA984207 Transform
30	145	100.0	112	2	AA967950 Human tra
31	145	100.0	112	3	AA92010 Human tra
32	145	100.0	112	4	AA835937 TGF-beta
33	145	100.0	112	5	AA851939 Human TGF
34	145	100.0	112	6	ABU08656 Human tra
35	145	100.0	112	6	ADH15598 Human bon
36	145	100.0	112	8	ABM79530 Human tra
37	145	100.0	114	2	AA839638 Human tra
38	145	100.0	115	4	AA873204 TGF-beta
39	145	100.0	115	6	ABG76033 Human TGF
40	145	100.0	116	2	AAW08176 TGF-beta
41	145	100.0	120	8	ADQ17006 Porcine T
42	145	100.0	120	8	ADQ17010 Porcine T
43	145	100.0	122	2	AAW08181 TGF-beta
44	145	100.0	124	2	AAW08177 TGF-beta
45	145	100.0	128	2	AAW08188 TGF-beta

## ALIGNMENTS

RESULT 1  
AA92983  
ID AA92983 standard; peptide: 23 AA.

AA92983;  
08-NOV-2000 (first entry)

Transforming growth factor inhibitory peptide P29.

Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1; competitive inhibitor; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; minotome; cirrhosis.

Homo sapiens.

WO200031135-A1.

02-JUN-2000.

23-NOV-1999; 99WO-BS000375.

24-NOV-1998; 98BS-00002465.

(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

Bzquerro Saenz JI, Laearte Sagacibelza JJ, Prieto Valcuna J; Borrás Cuesta F; WPI, 2000-411935/35.

Peptides that antagonize binding of transforming growth factor beta1, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.

Disclosure, Page 24; 86pp; Spanish.

The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-beta1 and/or its receptors. Peptides AA92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-beta1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis

XX Sequence 23 AA;

Query Match 100.0%; Score 145; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 4.3e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPPIYMSLDT 23  
|||  
DB 1 HEPKGYHANFCLGCPPIYMSLDT 23

RESULT 2  
AA92954  
ID AAY92954 standard; peptide; 23 AA.

XX AAY92954;

XX 08-NOV-2000 (first entry)

XX Transforming growth factor inhibitory peptide #10.

DE Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;  
KM competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KM extracellular matrix degradation inhibitor; mimotope; cirrhosis.

XX Homo sapiens.

OS WO200031135-A1.

PN 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

PF 24-NOV-1998; 98ES-00002465.

PR (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
PI Borras Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor beta1,  
PT useful for treatment of liver disease, especially cirrhosis, are partial  
sequences of the factor or its receptors.

XX Claim 11, Page 82; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
CC of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in  
CC vivo which have partial amino acid sequences identical, or similar, with  
CC those of TGF-beta1 and/or its receptors. Peptides AAY92954-Y93133 represent  
CC examples of the peptides of the invention. The peptides act by  
CC competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.  
CC they are inhibitors of stimulation of collagen synthesis in liver cells  
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
CC extracellular matrix. The peptides, their mimotopes and/or DNA (or  
CC expression systems) encoding the peptides are used for treatment of liver  
CC disease, specifically cirrhosis

XX Sequence 23 AA;

Query Match 100.0%; Score 145; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 4.3e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPPIYMSLDT 23  
|||  
DB 1 HEPKGYHANFCLGCPPIYMSLDT 23

RESULT 3

AAR90828  
ID AAR90828 standard; peptide; 50 AA.

XX AAR90828;

XX 25-MAR-2003 (revised)  
DT 25-JAN-1980 (first entry)

XX Pre-transforming growth factor beta 1 residues 252 to 302.

XX transforming growth factor beta 1; wound healing; recombinant production.

XX Homo sapiens.

OS US5482851-A.

PN 09-JAN-1996.

XX 05-NOV-1993; 93US-00147364.

PF 22-MAR-1985; 85US-00715142.

PR 13-MAR-1987; 87US-00025423.

PR 04-AUG-1989; 89US-00389929.

PR 04-MAR-1992; 92US-00845893.

XX (GETH ) GENENTECH INC.

XX Goeddel DV, Derynck RMA;

PI WPI; 1996-076891/08.

XX N-PSDB; AAT15721.

XX New recombinant human transforming growth factor-beta prods. - produced  
PT using Chinese hamster ovary cells, for use in diagnostic applications or  
in therapy.

XX Example 2; Fig 2; 26pp; English.

XX The transforming growth factor (TGF) beta 1 exon (residues 252 to 302)  
CC was identified using the "long probe" strategy used previously for TGF-  
CC alpha. Long oligonucleotides (T1572-23) designed on the basis of the  
CC partial protein sequence were used as hybridisation probes for the exon  
CC in a human genomic DNA library. The TGF beta 1 exon was then used as a  
CC probe for the isolation of TGF beta 1 cDNA (see AAT15270). DNA encoding  
CC TGF beta 1 is useful for the recombinant production of the protein, which  
CC is useful in, e.g. wound healing. (Updated on 25-MAR-2003 to correct PF  
CC field.)

XX Sequence 50 AA;

Query Match 100.0%; Score 145; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 8.7e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPPIYMSLDT 23  
|||  
DB 25 HEPKGYHANFCLGCPPIYMSLDT 47

RESULT 4

AAR04075  
ID AAR04075 standard; protein; 51 AA.

XX AAR04075;

XX 25-MAR-2003 (revised)

DT 31-OCT-2002 (revised)

XX 31-MAY-1989 (first entry)

XX Sequence of genomic fragment encoding a TGF-beta 1 exon.  
DE Transforming growth factor beta-3 (TGF beta 3); tumour cells;  
KM growth inhibition.

XX Homo sapiens.  
OS  
XX MO9912101-A.  
XX  
XX 14-DEC-1989.  
XX  
XX 08-JUN-1988; 88WO-US001945.  
XX  
XX 08-JUN-1988; 88WO-US001945.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Derynck RMA, Goeddel DV;  
XX  
XX WPI; 1990-007474/01.  
XX  
XX P-PSDB; AAR04075.  
XX  
XX Nucleotide sequence encoding transforming growth factor beta-3 - used as  
XX PT a probe, or to produce tgf beta-3, for growth inhibition of certain  
XX normal and neoplastic cells, e.g. A549.  
XX  
XX  
XX PS Disclosure; Fig 2; 61pp; English.  
XX  
XX This sequence encodes an exon of transforming growth factor-beta 1 (TGF-  
XX CC beta 1) polypeptide corresponding to AA's 288-338 of mature TGF-beta 1.  
XX CC The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-  
XX CC beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and  
XX CC neoplastic cell growth inhibition. (Updated on 31-OCT-2002 to add missing  
XX CC OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-  
XX CC MAR-2003 to correct PI field.)  
XX  
XX SQ Sequence 51 AA;

Query Match 100.0%; Score 145; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 8.9e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPYIWSLDT 23  
DB 25 HEPKGYHANFCLGCPYIWSLDT 47

RESULT 5  
AAW78788  
ID AAW78788 standard; protein; 51 AA.  
XX  
XX AAW78788;  
XX  
XX 25-MAR-2003 (revised)  
XX DT 21-DEC-1998 (first entry)  
XX  
XX Human transforming growth factor-beta fragment (aa288-338).  
XX DE  
XX Transforming growth factor-beta 1; TGF-beta 1; human.  
XX KW  
XX Homo sapiens.  
XX OS  
XX US5801231-A.  
XX  
XX 01-SEP-1998.  
XX  
XX 30-MAY-1995; 95US-00454468.  
XX  
XX 22-MAR-1985; 85US-00715142.  
XX PR 13-MAR-1987; 87US-00025423.  
XX PR 04-AUG-1989; 89US-00389929.  
XX PR 04-MAR-1992; 92US-00845893.  
XX PR 05-NOV-1993; 93US-00147364.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Derynck RMA, Goeddel DV;  
XX  
XX PI

XX WPI; 1998-494840/42.  
XX DR N-PSDB; AAV52936.  
XX  
XX  
XX PT DNA encoding transforming growth factor-beta precursor sequence - useful  
XX PT for analysis to perform manipulations to increase yield of recombinant  
XX PT production of the protein.  
XX  
XX PS Example 2; Fig 2; 26pp; English.  
XX

CC This polypeptide comprises amino acid residues 288-338 of human  
CC transforming growth factor-beta 1 precursor (preTGF-beta 1, see also  
CC CC AAW78785). It is encoded by an isolated fragment (see AAV52936) of the  
CC TGF-beta 1 gene. The invention relates to the recombinant production of  
CC TGF-beta. Nucleic acids encoding TGF-beta have been isolated and cloned  
CC into vectors which are replicated in bacteria and expressed in eukaryotic  
CC cells. TGF-beta recovered from transformed cells is used in known  
CC therapeutic applications. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
XX SQ Sequence 51 AA;

Query Match 100.0%; Score 145; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 8.9e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPYIWSLDT 23  
DB 25 HEPKGYHANFCLGCPYIWSLDT 47

RESULT 6  
ABB43879  
ID ABB43879 standard; peptide; 51 AA.  
XX  
XX ABB43879;  
XX  
XX 04-FEB-2002 (first entry)  
XX  
XX Peptide #11365 encoded by human foetal liver single exon probe.  
XX DE  
XX Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX KW  
XX Homo sapiens.  
XX OS  
XX WO200157277-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US000669.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
XX PR 26-MAY-2000; 2000US-0207456P.  
XX PR 30-JUN-2000; 2000US-00608408.  
XX PR 03-AUG-2000; 2000US-00632366.  
XX PR 21-SEP-2000; 2000US-0234687P.  
XX PR 27-SEP-2000; 2000US-0236359P.  
XX PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-483447/52.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX PT gene expression in human fetal liver.  
XX  
XX Claim 27; SEQ ID NO 36514; 639pp + Sequence listing; English.  
XX  
XX The invention relates to a single exon nucleic acid probe for measuring  
XX CC human gene expression in a sample derived from human foetal liver. The  
XX CC single exon nucleic acid probes may be used for predicting, measuring and  
XX CC displaying gene expression in samples derived from human fetal liver. The

CC present sequence is a peptide encoded by a single exon nucleic acid probe  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 51 AA;

Query Match 100.0%; Score 145; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 8,9e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPPIYWSLDT 23  
Db 25 HEPKGYHANFCLGCPPIYWSLDT 47

RESULT 7  
AAM37799  
ID AAM37799 standard; protein; 51 AA.

XX AAM37799;

DT 17-OCT-2001 (first entry)

XX Peptide #11836 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;

KM genetic disorder.

XX Homo sapiens.

OS WO200157272-A2.

XX PD 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX PF 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX (MOL- ) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 27; SEQ ID NO 38068; 654bp; English.

XX The present invention relates to single exon nucleic acid probes (SENP:

XX see AAI31315-AA157546). The present sequence is a peptide encoded by one

XX such probe. The probes are useful for producing a microarray for

XX predicting, measuring and displaying gene expression in samples derived

XX from human placenta. The probes are useful for antenatal diagnosis of

XX human genetic disorders

XX Sequence 51 AA;

Query Match 100.0%; Score 145; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 8,9e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPPIYWSLDT 23  
Db 25 HEPKGYHANFCLGCPPIYWSLDT 47

RESULT 8  
AAM77605  
ID AAM77605 standard; protein; 51 AA.

XX AAM77605;

DT 06-NOV-2001 (first entry)

XX Human bone marrow expressed probe encoded protein SEQ ID NO: 37911.

XX Human bone marrow expressed exon; gene expression analysis; probe;

KM microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

OS WO200157276-A2.

XX PD 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX PF 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX (MOL- ) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human bone marrow.

XX Example 4; SEQ ID NO 37911; 658bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX bone marrow. They can be used to measure gene expression in bone marrow

XX samples, which may enable the improved diagnosis and treatment of cancers

XX such as lymphoma, leukemia and myeloma. The present sequence is a

XX protein encoded by one of the probes of the invention

XX Sequence 51 AA;

XX Query Match 100.0%; Score 145; DB 4; Length 51;

XX Best Local Similarity 100.0%; Pred. No. 8,9e-12;

XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HEPKGYHANFCLGCPPIYWSLDT 23

Db 25 HEPKGYHANFCLGCPPIYWSLDT 47

RESULT 9  
ABG46640  
ID ABG46640 standard; peptide; 51 AA.

XX ABG46640;

DT 19-AUG-2002 (first entry)  
XX Human peptide encoded by genome-derived single exon probe SEQ ID 36305.

XX Human, single exon probe; asthma; lung cancer; COPD; ILD;

XX chronic obstructive pulmonary disease; interstitial lung disease;

XX familial idiopathic pulmonary fibrosis; neurofibromatosis;

XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

KM Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KM pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KM pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KM primary ciliary dyskinesia; pulmonary hypertension;  
 KM hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000665.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 XX  
 PR 30-JUN-2000; 2000US-00608408.  
 XX  
 PR 03-AUG-2000; 2000US-00632366.  
 XX  
 PR 21-SEP-2000; 2000US-0234687P.  
 XX  
 PR 27-SEP-2000; 2000US-0236359P.  
 XX  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 XX WPI; 2002-114183/15.  
 XX  
 PT Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples.  
 XX  
 PS Claim 27; SEQ ID NO 36305; 634bp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC; the novel set of probes which hybridize at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression in a sample  
 CC derived from human lung, comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exon should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORFs). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a peptide/protein encoded by a single exon probe of  
 CC the invention. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 51 AA;

Query Match 100.0%; Score 145; DB 5; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 8,9e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HEPKGYHANFCLGPPCYIWSLDT 23  
 Db 25 HEPKGYHANFCLGPPCYIWSLDT 47  
 RESULT 10  
 ID AAB68685 standard; protein; 60 AA.  
 XX  
 AC AAB68685;  
 XX  
 DT 03-MAY-2001 (first entry)  
 XX  
 DE Human TGFbeta1 protein #1.  
 XX  
 KW Human, transforming growth factor beta2; TGFbeta2; SELEX;  
 KW systemic evolution of ligands by exponential enrichment.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200109156-A1.  
 XX  
 PD 08-FEB-2001.  
 XX  
 PF 26-JUL-2000; 2000WO-US020397.  
 XX  
 PR 29-JUL-1999; 99US-00363939.  
 XX  
 PA (NEXS-) NEXSTAR PHARM INC.  
 XX  
 PI Pagratris N, Lochrie M, Gold L;  
 XX  
 XX WPI; 2001-218217/22.  
 XX  
 PT New RNA ligand to human transforming growth factor beta2, useful as  
 PT pharmaceuticals, diagnostics and as immunohistochemical reagents.  
 XX  
 PS Disclosure; Page 71; 178bp; English.  
 XX  
 CC The present invention relates to non-naturally occurring, high-affinity  
 CC RNA ligands to human transforming growth factor beta2 (TGFbeta2). The  
 CC oligonucleotide ligands were identified by the SELEX method (SELEX stands  
 CC for Systemic Evolution of Ligands by Exponential Enrichment). The  
 CC oligonucleotide ligands are useful in any process in which binding to  
 CC TGFbeta2 is required. The ligands may be useful as pharmaceuticals,  
 CC diagnostics, imaging agents and immunohistochemical reagents  
 XX  
 SQ Sequence 60 AA;  
 Query Match 100.0%; Score 145; DB 4; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 1e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HEPKGYHANFCLGPPCYIWSLDT 23  
 Db 34 HEPKGYHANFCLGPPCYIWSLDT 56  
 RESULT 11  
 ID AAM30331 standard; peptide; 62 AA.  
 XX  
 AC AAM30331;  
 XX  
 DT 11-FEB-1998 (first entry)  
 XX  
 DE Fragment of growth factor TGFbeta1.

KW Neurturin; human; haematopoietic cell; neuronal cell; stem cell; NT gene;  
 KW neurodegenerative disease; peripheral neuropathy; nervous system tumour;  
 KW amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease;  
 KW Huntington's disease; ischaemic stroke; acute brain injury; basopoenia;  
 KW acute spinal cord injury; multiple sclerosis; eosinopenia; lymphopenia;  
 KW monocytopenia; neutropenia; anaemia; thrombocytopenia; neuroblastoma;  
 KW antibody; obesity; therapy; transforming growth factor beta; TGfbeta1;  
 KW growth factor; hybrid protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9708196-A1.  
 XX  
 PD 06-MAR-1997.  
 XX  
 PF 27-AUG-1996; 96WO-US014065.  
 XX  
 PR 28-AUG-1995; 95US-00519777.  
 XX  
 PA (UNITW ) UNIV WASHINGTON.  
 XX  
 PI Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA;  
 DR WPI; 1997-179176/16.  
 XX  
 PT A novel growth factor Neurturin - used to treat neuro-degenerative and  
 PT haematopoietic cell degeneration diseases, e.g. Alzheimer's disease and  
 PT eosinopenia.  
 XX  
 PS Claim 93; Fig 17; 206pp; English.  
 XX  
 SQ AAM30331-W30353 represent human growth factor fragments that are used in  
 CC a hybrid polypeptide of the invention. These sequences form a hybrid with  
 CC the human neurturin (NT) fragment shown in AAM30378. NT promotes the  
 CC growth and differentiation of haematopoietic and neuronal cells, and  
 CC their stem cells. The NT gene and protein are used to prevent or treat  
 CC neurodegenerative diseases e.g. peripheral neuropathy, amyotrophic  
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's  
 CC disease, ischaemic stroke, acute brain injury, acute spinal cord injury,  
 CC nervous system tumour, multiple sclerosis and infection; and  
 CC haematopoietic cell degenerative diseases, e.g. eosinopenia, basopoenia,  
 CC lymphopenia, monocytopenia, neutropenia, anaemia, thrombocytopenia,  
 CC and stem cell insufficiencies. The NT protein and gene are also useful to  
 CC treat neuroblastomas. Antibodies against NT and oligonucleotides (used as  
 CC either probes or primers, corresponding to an exon of pre-pro-NT gene or  
 CC flanking a target sequence) can be used for detecting NT in a sample or  
 CC detecting mutations in the NT gene. Antisense sequences of the NT gene  
 CC are used to treat diseases promoted by NT expression e.g. obesity  
 CC  
 XX  
 SQ Sequence 62 AA;  
 Query Match 100.0%; Score 145; DB 2; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 HEPKGYHANFCLGCPFYIWSLDT 23  
 |||||  
 Db 20 HEPKGYHANFCLGCPFYIWSLDT 42  
 |||||  
 RESULT 12  
 AAR22135  
 ID AAR22135 standard; peptide; 65 AA.  
 XX  
 AC AAR22135;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 10-JUL-1992 (first entry)  
 XX  
 DB PDGI subunit b.  
 XX Platelet derived growth inhibitor alpha; TGF-beta; trypsin; pepsin;  
 KW cell proliferation; eczema; immunosuppressant.

XX  
 OS Homo sapiens.  
 XX  
 PN EP475719-A.  
 XX  
 PD 18-MAR-1992.  
 XX  
 PF 10-SEP-1991; 91EP-00308239.  
 XX  
 PR 11-SEP-1990; 90JP-00238944.  
 XX  
 PA (NAKA/) NAKAMURA T.  
 XX  
 PI Nakamura T, Nakamura T;  
 DR WPI; 1992-090304/12.  
 XX  
 PT New platelet-derived growth regulating peptide-alpha - used for treatment  
 PT of eczema, stimulation of bone growth and as immunosuppressant.  
 XX  
 PS Claim 2; Page 11; 21pp; English.  
 XX  
 SQ The peptide is subunit b of PDGI alpha. It can be obtd. by treating  
 CC transforming growth factor (TGF) beta with chymotrypsin or pepsin, or can  
 CC be isolated from human blood platelets or by recombinant expression of  
 CC DNA obtd. using RNA extd. from blood plasma. PDGI alpha is comprised of  
 CC subunits a, b and c bonded b-a-c. PDGI alpha can be used for controlling  
 CC cell proliferation without the cancerous activity (transformation  
 CC activity) associated with TGF-beta. PDGI- alpha can be used for  
 CC activation and acceleration of the proliferation of epithelium cells in  
 CC treating eczema, for stimulating osseous growth for bone formation or as  
 CC an immun- suppressant for immune diseases. See also AAR22134-6. (Updated  
 CC on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 65 AA;  
 Query Match 100.0%; Score 145; DB 2; Length 65;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 HEPKGYHANFCLGCPFYIWSLDT 23  
 |||||  
 Db 34 HEPKGYHANFCLGCPFYIWSLDT 56  
 |||||  
 RESULT 13  
 AAY16697  
 ID AAY16697 standard; peptide; 98 AA.  
 XX  
 AC AAY16697;  
 XX  
 DT 17-AUG-1999 (first entry)  
 DT 17-AUG-1999 (first entry)  
 XX  
 DE WO9914235 Seq ID No: 150.  
 KW Growth factor; GF; peraphrin; neuron growth; cellular degeneration;  
 KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma;  
 KW brain injury; spinal cord injury; nervous system tumour; infection;  
 KW multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin;  
 KW metabolic disease; diabetes; renal dysfunction; neurturin.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9914235-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 15-SEP-1998; 98WO-US019163.  
 XX  
 PR 16-SEP-1997; 97US-00931858.  
 XX  
 PA (UNITW ) UNIV WASHINGTON.



XX Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA, Klein R;  
PI Deaauvage F;  
XX WPI; 1999-244023/20.  
XX New isolated perlephin growth factor nucleic acids used to, e.g. promote  
PT neuronal growth.  
XX  
PS Disclosure; Page 175-176; 222pp; English.  
XX  
CC The invention relates to a novel isolated and purified growth factor (GF)  
CC that comprises perlephin or a fragment or a conservatively substituted  
CC variant. The perlephin GF polypeptides can promote the survival and  
CC growth of neurons and non-neuronal cells. The perlephin GF polypeptides  
CC or polynucleotides can be used for preventing or treating cellular  
CC degeneration or insufficiency, e.g. neuronal degeneration resulting from  
CC peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's  
CC disease, Parkinson's disease, Huntington's disease, ischemic stroke,  
CC acute brain injury, acute spinal cord injury, nervous system tumors,  
CC multiple sclerosis, or infection, hematopoietic cell degeneration or  
CC insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or  
CC stem-cell insufficiencies, cardiac muscle degeneration or insufficiency  
CC resulting from cardiomyopathy or congestive heart failure. They can also  
CC be used for treating e.g. peripheral nerve trauma or injury, exposure to  
CC neurotoxins, metabolic diseases such as diabetes or renal dysfunctions  
CC and damage caused by infectious agents. The GF can also be used for  
CC promoting the growth and/or differentiation of a cell in a culture  
CC medium. The antisense polynucleotides can be used for treating a disease  
CC condition mediated by expression of perlephin by a population of cells.  
CC The products can also be used for detection and diagnosis  
XX  
SQ Sequence 98 AA;  
Query Match 100.0%; Score 145; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.6e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 HEPKGYHANFCLGPGPYIWSLDT 23  
Db 20 HEPKGYHANFCLGPGPYIWSLDT 42  
RESULT 14  
AAAY92554  
ID AA92554 standard; peptide; 98 AA.  
XX  
AC AA92554;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE TGB-beta 1 finger-1-heel-finger-2 sequence.  
XX  
XX finger domain; heel region; BMP; TGF-beta family; protein refolding;  
KM fusion protein; osteopathic; antibacterial; cytoskeletal.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Domain 2..29  
PT /label= finger\_1  
FT 35..62  
FT /label= heel  
FT 65..94  
FT /label= finger\_2  
XX  
XX Domain  
XX  
XX WO200020449-A2.  
XX  
XX 13-APR-2000.  
XX  
XX 07-OCT-1999; 99WO-US023372.  
XX  
XX 07-OCT-1998; 98US-0103418P.  
XX  
XX 07-OCT-1998; 98US-0103418P.

PR 16-AUG-1999; 99US-00375333.  
XX  
XX (STYC ) STRYKER CORP.  
XX  
PI Oppermann H, Tai M, McCartney J;  
XX WPI; 2000-303743/26.  
XX  
XX A biologically active TGF-beta family member fusion protein competent to  
PT refold, comprising a C-terminal linked TGF-beta family protein.  
XX  
PS Disclosure; Page 137-138; 160pp; English.  
XX  
XX  
CC AA92554-82 show the finger 1, heel and finger 2 domains of TGF-beta  
CC superfamily members. These sequences can be used to form novel fusion  
CC proteins. Novel proteins comprise biologically active TGF-beta family  
CC member fusion proteins competent to refold under suitable refolding  
CC conditions. The fusion proteins comprise: (1) a TGF-beta family protein C  
CC -terminal seven cysteine domain, comprising finger 1, finger 2 and heel  
CC subdomains; and (2) a heterologous leader sequence domain operatively  
CC linked to the C-terminal domain. Truncations, heterodimers and mutants of  
CC these fusion proteins and methods of purifying the heterodimers are also  
CC claimed. The TGF-beta family proteins can be used to induce the full  
CC cascade of morphogenic events which culminate in skeletal tissue  
CC formation, including cartilage and endochondral bone formation. They are  
CC useful in the binding of fibrin and fibronectin to the implanted matrix,  
CC chemotaxis of cells, proliferation of fibroblasts, differentiation into  
CC chondroblasts, cartilage formation, vascular invasion, bone formation,  
CC remodeling, and bone marrow differentiation. The proteins have improved  
CC physical properties such as solubility and stability, improved biological  
CC activity, including altered receptor binding and improved targeting  
CC capabilities  
XX  
SQ Sequence 98 AA;  
Query Match 100.0%; Score 145; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.6e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 HEPKGYHANFCLGPGPYIWSLDT 23  
Db 20 HEPKGYHANFCLGPGPYIWSLDT 42  
RESULT 15  
AAB09519  
ID AAB09519 standard; protein; 98 AA.  
XX  
AC AAB09519;  
XX  
DT 11-SEP-2000 (first entry)  
XX  
XX Human TGF-beta 1, SEQ ID NO:40.  
XX  
XX TGF-beta superfamily; transforming growth factor-beta;  
KM developmental regulation; finger 2 subdomain; basic region;  
KM protein refolding; stability; solubility; osteogenic protein; OP;  
KM bone morphogenetic protein; BMP; growth/differentiation factor; GDF;  
KM inhibin; tissue morphogenesis; regeneration; bone; dental tissue;  
KM connective tissue; cartilage; vulnery.  
XX  
XX Homo sapiens.  
XX  
XX WO200020607-A2.  
XX  
XX 13-APR-2000.  
XX  
XX 07-OCT-1999; 99WO-US023371.  
XX  
XX 07-OCT-1998; 98US-0103418P.  
XX  
XX 16-AUG-1999; 99US-00374958.  
XX  
XX (STYC ) STRYKER CORP.

XX Oppermann H, Tai M, McCartney J;  
 XX WPI: 2000-303787/26.  
 DR N-PSDB; AAA38544.  
 XX

PT Transforming growth factor-beta superfamily member mutant induces tissue  
 PT morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental  
 PT tissue and connective tissue and comprises a substitution in a region of  
 PT the finger 2 domain.

XX Claim 14; Page 140; 162pp; English.  
 PS

XX The invention relates to mutant TGF-beta (transforming growth factor-  
 CC beta) superfamily members. These mutants comprise one or more amino acid  
 CC substitutions in the base region of the finger 2 subdomain, and a C-  
 CC terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger  
 CC 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an  
 CC amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g.,  
 CC Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-  
 CC beta superfamily proteins regulate developmental processes and include  
 CC proteins such as the osteogenic proteins (OPs), bone morphogenetic  
 CC proteins (BMPs), growth/differentiation factors (GDFs) and inhibitors.  
 CC Specific examples of TGF-beta superfamily mutants encompassed by the  
 CC invention are the finger 2 subdomain mutants of human osteogenic protein-  
 CC 1 (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins are used for  
 CC inducing tissue morphogenesis in bone, non-mineralised skeletal tissue,  
 CC dental tissue, connective tissue, brain, liver and nerve tissue. The  
 CC proteins can be used in conjunction with a biocompatible matrix e.g.,  
 CC collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone,  
 CC cartilage and/or other mineralised skeletal or connective tissues e.g.,  
 CC ligament, tendon, muscle, fibrocartilage, joint capsule and  
 CC intervertebral discs. The OP-1 mutants can be used to repair diseased or  
 CC damaged mammalian tissue and to prevent or substantially inhibit  
 CC immune/inflammatory response-mediated tissue damage and scar tissue  
 CC formation following an injury. Compared to the wild-type TGF-beta  
 CC superfamily members, the mutant proteins have improved in vitro refolding  
 CC properties in a pH range of 6-9, increased solubility in aqueous solution  
 CC and improved stability and/or activity. Sequences AAB09519-B09542 and  
 CC AAB09553-B09558 represent a variety of wild-type TGF-beta superfamily  
 CC proteins referred to in the specification  
 XX

XX Sequence 98 AA;  
 SQ

Query Match 100.0%; Score 145; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGPCPYIWSLDT 23  
 |||||  
 DB 20 HEPKGYHANFCLGPCPYIWSLDT 42

Search completed: June 14, 2005, 15:46:23  
 Job time : 131.808 secs

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## OM protein - protein search, using sw model

Run on: June 14, 2005, 15:46:34 ; Search time 34.0577 Seconds  
(without alignments)  
50.412 Million cell updates/sec

Title: US-09-831-253F-10  
Sequence: 1 HEPKGYHANFCLGPPCYIWSLDT 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Issued Patents, AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfill1es1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	145	100.0	51	5168051-4	Patent No. 5168051
2	145	100.0	51	5168051-4	Patent No. 5168051
3	145	100.0	60	US-09-363-939A-122	Sequence 122, App
4	145	100.0	60	US-09-791-301-122	Sequence 122, App
5	145	100.0	70	US-09-848-664A-9	Sequence 9, Appl
6	145	100.0	98	US-08-478-097A-1	Sequence 1, Appl
7	145	100.0	98	US-08-931-858E-150	Sequence 150, App
8	145	100.0	98	US-08-981-739-150	Sequence 150, App
9	145	100.0	98	US-09-128-026-150	Sequence 150, App
10	145	100.0	98	US-09-496-398-1	Sequence 1, Appl
11	145	100.0	98	US-09-220-616-150	Sequence 150, App
12	145	100.0	98	US-09-374-958C-40	Sequence 40, App
13	145	100.0	98	US-09-220-527-150	Sequence 150, App
14	145	100.0	98	US-09-220-441-150	Sequence 150, App
15	145	100.0	112	US-07-979-441-1	Sequence 1, Appl
16	145	100.0	112	US-08-197-792-36	Sequence 36, Appl
17	145	100.0	112	US-08-486-057B-41	Sequence 41, Appl
18	145	100.0	112	US-08-459-850-36	Sequence 36, Appl
19	145	100.0	112	US-08-459-214-36	Sequence 36, Appl
20	145	100.0	112	US-08-470-837-30	Sequence 30, Appl
21	145	100.0	112	US-08-789-588-41	Sequence 41, Appl
22	145	100.0	112	US-08-410-573-1	Sequence 1, Appl
23	145	100.0	112	US-09-123-233-2	Sequence 2, Appl
24	145	100.0	112	US-08-927-433-5	Sequence 5, Appl
25	145	100.0	112	US-08-868-452-30	Sequence 30, Appl
26	145	100.0	112	US-09-095-637D-1	Sequence 1, Appl
27	145	100.0	112	PCT-US93-03068-1	Sequence 1, Appl

28	145	100.0	114	1	US-08-481-377-23	Sequence 23, Appl
29	145	100.0	114	2	US-08-491-835-21	Sequence 21, Appl
30	145	100.0	114	3	US-09-153-733A-23	Sequence 23, Appl
31	145	100.0	114	3	US-08-946-092A-21	Sequence 21, Appl
32	145	100.0	114	3	US-09-172-062-21	Sequence 21, Appl
33	145	100.0	114	3	US-08-624-635-22	Sequence 22, Appl
34	145	100.0	114	3	US-09-301-520D-21	Sequence 21, Appl
35	145	100.0	114	3	US-09-389-705-23	Sequence 23, Appl
36	145	100.0	114	5	PCT-US94-00666-23	Sequence 23, Appl
37	145	100.0	114	5	PCT-US94-00685-21	Sequence 21, Appl
38	145	100.0	115	1	US-08-581-529B-19	Sequence 19, Appl
39	145	100.0	115	1	US-08-455-559-25	Sequence 25, Appl
40	145	100.0	115	2	US-08-525-596B-29	Sequence 29, Appl
41	145	100.0	115	2	US-08-581-528A-19	Sequence 19, Appl
42	145	100.0	115	3	US-09-097-616-19	Sequence 19, Appl
43	145	100.0	115	3	US-09-177-860A-29	Sequence 29, Appl
44	145	100.0	115	3	US-09-145-060-25	Sequence 25, Appl
45	145	100.0	115	4	US-09-378-238-39	Sequence 39, Appl

## ALIGNMENTS

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RESULT 1
5168051-4
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO:4:
; LENGTH: 51
5168051-4

Query Match
Best Local Similarity 100.0%; Score 145; DB 6; Length 51;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 HEPKGYHANFCLGPPCYIWSLDT 23
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25 HEPKGYHANFCLGPPCYIWSLDT 47
|||||

RESULT 2
5168051-4
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO:4:
; LENGTH: 51
5168051-4

Query Match
Best Local Similarity 100.0%; Score 145; DB 6; Length 51;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 HEPKGYHANFCLGPPCYIWSLDT 23
|||||
25 HEPKGYHANFCLGPPCYIWSLDT 47
|||||

RESULT 3
US-09-363-939A-122
; Sequence 122, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratlis, Nikos
```

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; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-363-939A-122
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```
Query Match          100.0%; Score 145; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 HEPKGYHANFCLGCPYIWSLDT 23
        |||||||
Db      34 HEPKGYHANFCLGCPYIWSLDT 56
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RESULT 4
US-09-791-301-122
; Sequence 122, Application US/09791301
; Patent No. 6713616
; GENERAL INFORMATION:
; APPLICANT: Pagratlis, Nikos
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; FILE REFERENCE: NEX 87/C
; CURRENT APPLICATION NUMBER: US/09/791,301
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
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; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-791-301-122
```

```
Query Match          100.0%; Score 145; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 HEPKGYHANFCLGCPYIWSLDT 23
        |||||||
Db      34 HEPKGYHANFCLGCPYIWSLDT 56
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RESULT 5
US-09-848-664A-9
; Sequence 9, Application US/09848664A
; Patent No. 6723344
; GENERAL INFORMATION:
; APPLICANT: Sakiyama-Eibert, Shelly E.
; APPLICANT: Hubbell, Jeffrey A.
; TITLE OF INVENTION: Controlled Release of No. 6723344-Heparin Binding Growth
; FILE REFERENCE: ETH 108
; CURRENT APPLICATION NUMBER: US/09/848,664A
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US/09/298,084A
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-664A-9
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Query Match          100.0%; Score 145; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 HEPKGYHANFCLGCPYIWSLDT 23
        |||||||
Db      34 HEPKGYHANFCLGCPYIWSLDT 56
```

```

RESULT 6
US-08-478-097A-1
; Sequence 1, Application US/08478097A
; Patent No. 6040431
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: SMART, JOHN
; TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B
; TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HUMWITZ &
; ADDRESSEE: THIBEAULT, LLP
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,097A
```

FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER ESQ, EDMUND R  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-080  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..98  
OTHER INFORMATION: /note="TGF-B1 SEQUENCE"  
US-08-478-097A-1

Query Match 100.0%; Score 145; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 4.2e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPPIYMSLDT 23  
Db 20 HEPKGYHANFCLGCPPIYMSLDT 42

RESULT 7  
US-08-931-858E-150  
Sequence 150, Application US/08931858E  
Patent No. 6222022  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, EUGENE M  
APPLICANT: MILBRANDT, JEFFREY D  
APPLICANT: KOTZBAUER, PAUL T  
APPLICANT: LAMPE, PATRICIA A  
APPLICANT: KLEIN, ROBERT  
APPLICANT: DESAUVAGE, FRED  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
NUMBER OF SEQUENCES: 239  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MO  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931.858E  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971486  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 314-727-5188  
TELEFAX: 314-727-6092  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-08-931-858E-150

Query Match 100.0%; Score 145; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 4.2e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPPIYMSLDT 23  
Db 20 HEPKGYHANFCLGCPPIYMSLDT 42

RESULT 8  
US-08-981-739-150  
Sequence 150, Application US/08981739  
Patent No. 6232449  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
APPLICANT: MILBRANDT, JEFFREY D.  
APPLICANT: KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/981.739  
FILING DATE: 31-Aug-1998  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/03461  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 150:  
US-08-981-739-150

Query Match 100.0%; Score 145; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 4.2e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPPIYMSLDT 23  
Db 20 HEPKGYHANFCLGCPPIYMSLDT 42

RESULT 9  
US-09-128-026-150  
Sequence 150, Application US/09128026  
Patent No. 6403335  
GENERAL INFORMATION:

APPLICANT: JOHNSON JR., EUGENE M.  
APPLICANT: MILBRANDT, JEFFREY D.  
APPLICANT: KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/128,026  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-128-026-150

Query Match 100.0%; Score 145; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 4.2e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYMSLDT 23  
Db 20 HEPKGYHANFCLGCPPIYMSLDT 42

RESULT 10  
US-09-496-398-1  
Sequence 1, Application US/09496398  
Patent No. 6479643  
GENERAL INFORMATION:  
APPLICANT: KECK, PETER  
APPLICANT: SMART, JOHN  
TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B  
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &  
ADDRESSEE: THIBEAULT, LLP  
STREET: 125 HIGH STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/496,398  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,097  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER ESQ, EDMUND R  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: STK-059CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..98  
OTHER INFORMATION: /note= "TGF-B1 SEQUENCE"  
US-09-496-398-1

Query Match 100.0%; Score 145; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 4.2e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYMSLDT 23  
Db 20 HEPKGYHANFCLGCPPIYMSLDT 42

RESULT 11  
US-09-220-616-150  
Sequence 150, Application US/09220616  
Patent No. 6645937  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
APPLICANT: MILBRANDT, JEFFREY D.  
APPLICANT: KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/220,616  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/981,739  
FILING DATE: 31-Aug-1998  
APPLICATION NUMBER: PCT/US97/03461  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-220-616-150

Query Match 100.0%; Score 145; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 4.2e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPYIWSLDT 23  
|||  
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 12  
US-09-374-958C-40  
Sequence 40, Application US/09374958C  
Patent No. 6677432  
GENERAL INFORMATION:  
APPLICANT: Stryker Corporation  
TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including  
FILE REFERENCE: STK-076  
CURRENT APPLICATION NUMBER: US/09/374,958C  
CURRENT FILING DATE: 1999-08-16  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: PatentIn version 2.0  
SEQ ID NO 40  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: TGF-beta1  
US-09-374-958C-40

Query Match 100.0%; Score 145; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 4.2e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPYIWSLDT 23  
|||  
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 13  
US-09-220-527-150  
Sequence 150, Application US/09220527  
Patent No. 6692943  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
MILBRANDT, JEFFREY D.  
KOTZBAUER, PAUL T.  
LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/220,527

FILING DATE: 24-Dec-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/981,739  
FILING DATE: 31-Aug-1998  
APPLICATION NUMBER: PCT/US97/03461  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 150:  
US-09-220-527-150

Query Match 100.0%; Score 145; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 4.2e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPYIWSLDT 23  
|||  
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 14  
US-09-220-407-150  
Sequence 150, Application US/09220407  
Patent No. 6716600  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, EUGENE M.  
MILBRANDT, JEFFREY D.  
APPLICANT: KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
APPLICANT: KLEIN, ROBERT  
APPLICANT: DESAUVAGE, FRED  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
NUMBER OF SEQUENCES: 239  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MO  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/220,407  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,858  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971486  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 314-727-5188  
TELEFAX: 314-727-6092  
INFORMATION FOR SEQ ID NO: 150:

Job time : 34.0577 secs

SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-220-407-150

Query Match 100.0%; Score 145; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 4.2e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPYIWSLDT 23  
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 15  
US-07-979-441-1  
; Sequence 1, Application US/07979441  
; Patent No. 5462925  
; GENERAL INFORMATION:  
; APPLICANT: OGAMA, YASUSHI  
; APPLICANT: SCHMIDT, DAVID  
; APPLICANT: DASCH, JAMES  
; TITLE OF INVENTION: NOVEL BETA-TYPE TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/979,441  
; FILING DATE: 19921120  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/614,306  
; FILING DATE: 16-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CIOTTI, THOMAS E.  
; REGISTRATION NUMBER: 21,013  
; REFERENCE/DOCKET NUMBER: 220952024800  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-979-441-1

Query Match 100.0%; Score 145; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. NO. 4.7e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPYIWSLDT 23  
Db 34 HEPKGYHANFCLGCPYIWSLDT 56

Search completed: June 14, 2005, 16:10:14



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## OM protein - protein search, using sw model

Run on: June 14, 2005, 15:51:20 ; Search time 120.308 Seconds  
(without alignments)  
73.285 Million cell updates/sec

Title: US-09-831-253F-10  
Perfect score: 145  
Sequence: 1 HEPKGYHANFCLGPCPYIWSLDT 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09C\_NEW\_PUB.pep.\*
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- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US10F\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	145	100.0	51	9	US-09-864-761-47871
2	145	100.0	60	10	US-09-791-301-122
3	145	100.0	60	16	US-10-812-642-122
4	145	100.0	70	9	US-09-848-664-9
5	145	100.0	98	14	US-10-187-394-1
6	145	100.0	112	9	US-09-813-271B-2
7	145	100.0	112	15	US-10-366-345-54
8	145	100.0	112	17	US-10-872-198-104
9	145	100.0	113	9	US-09-813-398-13
10	145	100.0	113	16	US-10-826-324-13
11	145	100.0	114	9	US-09-389-705-23

12	145	100.0	114	9	US-09-813-459-22	Sequence 22, Appl
13	145	100.0	114	13	US-10-115-406-21	Sequence 21, Appl
14	145	100.0	114	14	US-10-154-333-23	Sequence 23, Appl
15	145	100.0	114	16	US-10-704-223-21	Sequence 21, Appl
16	145	100.0	115	9	US-09-859-211-47	Sequence 47, Appl
17	145	100.0	115	9	US-09-880-708-25	Sequence 25, Appl
18	145	100.0	115	10	US-09-872-856-47	Sequence 47, Appl
19	145	100.0	115	14	US-10-335-483-29	Sequence 29, Appl
20	145	100.0	115	15	US-10-463-973-47	Sequence 47, Appl
21	145	100.0	115	15	US-10-693-536-19	Sequence 19, Appl
22	145	100.0	115	16	US-10-758-210-19	Sequence 19, Appl
23	145	100.0	139	13	US-10-002-278-8	Sequence 8, Appl
24	145	100.0	185	16	US-10-781-866-52	Sequence 52, Appl
25	145	100.0	218	16	US-10-781-866-51	Sequence 51, Appl
26	145	100.0	315	10	US-09-214-592-25	Sequence 25, Appl
27	145	100.0	390	9	US-09-756-283A-23	Sequence 23, Appl
28	145	100.0	390	10	US-09-214-592-23	Sequence 20, Appl
29	145	100.0	390	10	US-09-214-592-20	Sequence 20, Appl
30	145	100.0	390	10	US-09-214-592-26	Sequence 26, Appl
31	145	100.0	390	10	US-09-214-592-28	Sequence 28, Appl
32	145	100.0	390	10	US-09-214-592-33	Sequence 29, Appl
33	145	100.0	390	10	US-09-214-592-33	Sequence 33, Appl
34	145	100.0	390	14	US-10-087-268-2	Sequence 2, Appl
35	145	100.0	390	14	US-10-087-268-5	Sequence 5, Appl
36	145	100.0	390	14	US-10-276-947-1	Sequence 1, Appl
37	145	100.0	390	14	US-10-131-985-13	Sequence 13, Appl
38	145	100.0	390	15	US-10-366-345-46	Sequence 46, Appl
39	145	100.0	390	16	US-10-746-845-38	Sequence 38, Appl
40	145	100.0	390	16	US-10-688-845-12	Sequence 12, Appl
41	145	100.0	390	17	US-10-741-600-1307	Sequence 1307, Ap
42	145	100.0	390	17	US-10-741-600-1308	Sequence 1308, Ap
43	145	100.0	390	17	US-10-901-417-13	Sequence 13, Appl
44	145	100.0	391	10	US-09-214-592-17	Sequence 17, Appl
45	145	100.0	391	17	US-10-741-600-1309	Sequence 1309, Ap

## ALIGNMENTS

RESULT 1  
US-09-864-761-47871  
; Sequence 47871, Application US/09864761  
; Patent No. US20020048763A1  
GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aecm1ca-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263,6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47871
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011462.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.8
; OTHER INFORMATION: EST HUMAN HIT: BE737006.1, EVALUE 4.00e-28
; OTHER INFORMATION: SWISSPROT HIT: O19011, EVALUE 3.00e-29
US-09-864-761-47871

Query Match          100.0%; Score 145; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 2,7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HEPKGYANFCLGCPYIWSLDT 23
Db      25 HEPKGYANFCLGCPYIWSLDT 47

RESULT 2
US-09-791-301-122
; Sequence 122, Application US/09791301
; Publication No. US20030064943A1
; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; FILE REFERENCE: NEX 87/C
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
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; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-791-301-122

Query Match          100.0%; Score 145; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 3,1e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HEPKGYANFCLGCPYIWSLDT 23
Db      34 HEPKGYANFCLGCPYIWSLDT 56

RESULT 3
US-10-812-642-122
; Sequence 122, Application US/10812642
; Publication No. US20040258656A1
; GENERAL INFORMATION:
; APPLICANT: Pagratie, Nikos
; APPLICANT: Lochrie, Michael
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; FILE REFERENCE: NEX87
; CURRENT FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: US/09/363,939A
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-10-812-642-122

Query Match          100.0%; Score 145; DB 16; Length 60;
Best Local Similarity 100.0%; Pred. No. 3,1e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HEPKGYANFCLGCPYIWSLDT 23
Db      34 HEPKGYANFCLGCPYIWSLDT 56

RESULT 4
US-09-848-664-9
; Sequence 9, Application US/09848664
; Patent No. US20020146414A1
; GENERAL INFORMATION:
; APPLICANT: Sakiyama-Eibert, Shelly E.
; APPLICANT: Hubbell, Jeffrey A.
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TITLE OF INVENTION: Controlled Release of No. US2002014641A1-Heparin Binding Growth  
; TITLE OF INVENTION: Factors from Heparin Containing Matrices  
; FILE REFERENCE: ETH 108  
; CURRENT APPLICATION NUMBER: US/09/848,664  
; PRIOR APPLICATION NUMBER: 2001-05-03  
; PRIOR FILING DATE: 1999-04-22  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO: 9  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-848-664-9

Query Match 100.0%; Score 145; DB 9; Length 70;  
Best Local Similarity 100.0%; Pred. No. 3.5e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23  
Db 34 HEPKGYHANFCLGCPYIWSLDT 56

RESULT 5  
US-10-187-394-1  
; Sequence 1, Application US/10187394  
; Publication No. US20030176667A1  
; GENERAL INFORMATION:  
; APPLICANT: KECK, PETER  
; APPLICANT: SMART, JOHN  
; TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B  
; TITLE OF INVENTION: SUPERFAMILY (MORPHONS)  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &  
; ADDRESS: THIBEAULT, LLP  
; STREET: 125 HIGH STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/187,394  
; FILING DATE: 28-JUNE-2002  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/496,398  
; FILING DATE: 02-FEB-2000  
; CLASSIFICATION:  
; APPLICATION NUMBER: US 08/478,097  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PITCHER ESQ, EDMUND R  
; REGISTRATION NUMBER: 27,829  
; REFERENCE/DOCKET NUMBER: STK-059CN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-248-7000  
; TELEFAX: 617-248-7100  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:

NAME/KEY: Protein  
; LOCATION: 1..98  
; OTHER INFORMATION: /note="TGF-B1 SEQUENCE"  
US-10-187-394-1

Query Match 100.0%; Score 145; DB 14; Length 98;  
Best Local Similarity 100.0%; Pred. No. 4.7e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23  
Db 20 HEPKGYHANFCLGCPYIWSLDT 42

RESULT 6  
US-09-813-271B-2  
; Sequence 2, Application US/09813271B  
; Patent No. US20020115834A1  
; GENERAL INFORMATION:  
; APPLICANT: (A) Nisco Cerletti  
; TITLE OF INVENTION: New process for the production of  
; biologically active protein  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. US20020115834A1artis Patent Department  
; STREET: 564 Morris Avenue  
; CITY: Summit  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07901  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/813,271B  
; FILING DATE: 20-Mar-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/02719  
; FILING DATE: 12-Jul-95  
; APPLICATION NUMBER: EPO 94810439.3  
; FILING DATE: 25-Jul-94  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pfeiffer, Hessa J.  
; REGISTRATION NUMBER: 22640  
; REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 522-6940  
; TELEFAX: (908) 522-6955  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-813-271B-2

Query Match 100.0%; Score 145; DB 9; Length 112;  
Best Local Similarity 100.0%; Pred. No. 5.3e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23  
Db 34 HEPKGYHANFCLGCPYIWSLDT 56

RESULT 7  
US-10-366-345-54  
; Sequence 54, Application US/10366345  
; Publication No. US20030224501A1

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; GENERAL INFORMATION:
; APPLICANT: Young, et al.
; TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and
; FILE REFERENCE: PT189
; CURRENT APPLICATION NUMBER: US/10/366,345
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-345-54

Query Match          100.0%; Score 145; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HEPKGYHANFCLGPGPYIWSLDT 23
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Db      34 HEPKGYHANFCLGPGPYIWSLDT 56

RESULT 8
US-10-872-198-104
; Sequence 104, Application US/10872198
; Publication No. US2005002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andraea SCHEIDIG
; APPLICANT: Christian VOETSMEIER
; APPLICANT: Ulrich Ketting
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000204
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-104

Query Match          100.0%; Score 145; DB 17; Length 112;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HEPKGYHANFCLGPGPYIWSLDT 23
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Db      34 HEPKGYHANFCLGPGPYIWSLDT 56

RESULT 9
US-09-813-398-13
; Sequence 13, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
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; APPLICANT: Mariusz W. Skudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: USFMD.003C1
; CURRENT APPLICATION NUMBER: US/09/813,398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-813-398-13

Query Match          100.0%; Score 145; DB 9; Length 113;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HEPKGYHANFCLGPGPYIWSLDT 23
      |||
Db      35 HEPKGYHANFCLGPGPYIWSLDT 57

RESULT 10
US-10-826-324-13
; Sequence 13, Application US/10826324
; Publication No. US20040265972A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Mariusz W. Skudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: USFMD.003C1
; CURRENT APPLICATION NUMBER: US/10/826,324
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US/09/813,398
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-10-826-324-13

Query Match          100.0%; Score 145; DB 16; Length 113;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HEPKGYHANFCLGPGPYIWSLDT 23
      |||
Db      35 HEPKGYHANFCLGPGPYIWSLDT 57

RESULT 11
US-09-389-705-23
; Sequence 23, Application US/09389705
; Publication No. US20010018509A1
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLAY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
```

CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/389,705  
FILING DATE: 03-Sep-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/153,733  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: WETHERELL, JR., Ph.D., JOHN R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD2279 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5100  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta 1  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..114  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-389-705-23  
Query Match 100.0%; Score 145; DB 9; Length 114;  
Best Local Similarity 100.0%; Pred. No. 5,4e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 HEPKGYHANFCLGCPYIWSLDT 23  
Db 36 HEPKGYHANFCLGCPYIWSLDT 58  
RESULT 12  
US-09-813-459-22  
Sequence 22, Application US/09813459  
Patent No. US20020107369A1  
GENERAL INFORMATION:  
APPLICANT: Lee, Se-Jin  
Cunningham, No. US20020107369A1  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/813,459  
FILING DATE: 20-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/624,635  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D., John R.,  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-3054  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: TGF-beta-1  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..114  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-813-459-22  
Query Match 100.0%; Score 145; DB 9; Length 114;  
Best Local Similarity 100.0%; Pred. No. 5,4e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 HEPKGYHANFCLGCPYIWSLDT 23  
Db 36 HEPKGYHANFCLGCPYIWSLDT 58  
RESULT 13  
US-10-115-406-21  
Sequence 21, Application US/10115406  
Publication No. US20020127612A1  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
APPLICANT: Lee, Se-Jin  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9  
FILE REFERENCE: JH01190-3  
CURRENT APPLICATION NUMBER: US/10/115,406  
CURRENT FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: 09/301,520  
PRIOR FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: US 09/172,062  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: US 08/491,835  
PRIOR FILING DATE: 1995-10-23  
PRIOR APPLICATION NUMBER: PCT/US94/00685  
PRIOR FILING DATE: 1994-01-12  
PRIOR APPLICATION NUMBER: US 08/003,303  
PRIOR FILING DATE: 1993-01-12  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 21  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-115-406-21  
Query Match 100.0%; Score 145; DB 13; Length 114;  
Best Local Similarity 100.0%; Pred. No. 5,4e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 HEPKGYHANFCLGCPYIWSLDT 23  
Db 36 HEPKGYHANFCLGCPYIWSLDT 58  
RESULT 14  
US-10-154-333-23

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; Sequence 23, Application US/10154333
; Publication No. US20030109684A1
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/154,333
; FILING DATE: 21-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/389,705
; FILING DATE: 03-Sep-1999
; APPLICATION NUMBER: 09/153,733
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph. D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta 1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
; US-10-154-333-23

Query Match 100.0%; Score 145; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 5,4e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGPCPYIWSLDT 23
Db 36 HEPKGYHANFCLGPCPYIWSLDT 58

RESULT 15
US-10-704-223-21
; Sequence 21, Application US/10704223
; Publication No. US20040152143A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; FILE REFERENCE: JH01190-7
; CURRENT APPLICATION NUMBER: US/10/704,223
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 10/115,406
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US 09/301,520
; PRIOR FILING DATE: 1999-04-28
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; PRIOR APPLICATION NUMBER: US 09/172,062
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/491,835
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: PCT/US94/00685
; PRIOR FILING DATE: 1994-01-12
; PRIOR APPLICATION NUMBER: US 08/003,303
; PRIOR FILING DATE: 1993-01-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-704-223-21

Query Match 100.0%; Score 145; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 5,4e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGPCPYIWSLDT 23
Db 36 HEPKGYHANFCLGPCPYIWSLDT 58

Search completed: June 14, 2005, 16:14:52
Job time : 120.308 secs
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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 14, 2005, 15:35:40 ; Search time 25.6538 Seconds  
(without alignments)  
86.263 Million cell updates/sec

Title: US-09-831-253F-10  
Perfect score: 145  
Sequence: 1 HEPKGYHANFCLGCPPIWMSLDT 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	145	100.0	130	2	148196	transforming growth
2	145	100.0	315	2	A40057	transforming growth
3	145	100.0	390	1	WFMU2	transforming growth
4	145	100.0	390	1	WFMU2	transforming growth
5	145	100.0	390	2	A26960	transforming growth
6	145	100.0	390	2	JC4023	transforming growth
7	145	100.0	390	2	A27512	transforming growth
8	145	100.0	390	2	146463	transforming growth
9	145	100.0	390	2	SI0219	transforming growth
10	145	100.0	391	2	S01413	transforming growth
11	128	88.3	373	2	A41918	transforming growth
12	124	85.5	412	2	A39489	transforming growth
13	123	84.8	382	2	B61036	transforming growth
14	117	80.7	112	2	A61439	transforming growth
15	117	80.7	413	1	WFLB2	transforming growth
16	117	80.7	414	1	WFMU2	transforming growth
17	117	80.7	414	1	WFMU2	transforming growth
18	117	80.7	414	2	A31249	transforming growth
19	117	80.7	442	2	B12449	transforming growth
20	112	77.2	409	2	S01825	transforming growth
21	112	77.2	410	2	A41397	transforming growth
22	112	77.2	412	2	A36169	transforming growth
23	111	76.6	410	2	A55706	transforming growth
24	109	75.2	412	2	A34939	transforming growth
25	68	46.9	115	2	PNO504	activin beta A chain
26	68	46.9	360	2	A28619	Vg1 embryonic growth
27	68	46.9	424	1	B40905	inhibin beta-A chain
28	68	46.9	424	1	S31440	inhibin beta-A chain
29	68	46.9	424	1	WFMU2	inhibin beta-A chain

30	68	46.9	425	1	S50898	inhibin beta-A cha
31	68	46.9	425	2	147072	inhibin beta-A cha
32	68	46.9	426	1	B24248	inhibin beta-A cha
33	67	46.2	102	2	A36192	inhibin beta-A cha
34	64	44.1	352	2	JC2456	inhibin beta-A cha
35	62	42.8	366	2	A45402	transforming growt
36	62	42.8	366	2	A46607	transforming growt
37	61	42.1	351	2	A44201	bone morphogenetic
38	61	42.1	352	2	S70580	bone morphogenetic
39	61	42.1	352	2	JC5366	activin beta C pre
40	61	42.1	393	2	S37073	bone morphogenetic
41	61	42.1	394	2	S45355	bone morphogenetic
42	61	42.1	396	1	EMH02	bone morphogenetic
43	61	42.1	398	2	JH0688	bone morphogenetic
44	61	42.1	398	2	JH0687	bone morphogenetic
45	60	41.4	367	2	JC4151	activin beta D cha

## ALIGNMENTS

RESULT 1  
148196  
transforming growth factor beta-1 precursor - golden hamster (fragment)  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 02-Jul-1996 #sequence\_revision 04-Oct-1996 #text\_change 09-Jul-2004  
C:Accession: 148196  
R:Wong, D.T.; Donoff, R.B.; Yang, J.; Song, B.Z.; Matosian, K.; Nagura, N.; Elovic, A.;  
Am. J. Pathol. 143, 130-142, 1993  
A:Title: Sequential expression of transforming growth factors alpha and beta 1 by eosino-  
A:Reference number: 148196; MUID:93304479; PMID:8317544  
A:Accession: 148196  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-130 <RES>  
A:Cross-references: UNIPROT:Q08714; EMBL:X60296; NID:G396177; PIDN:CAA42838.1; PID:G3961  
C:Superfamily: inhibin

Query Match  
Best Local Similarity 100.0%; Score 145; DB 2; Length 130;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 52 HEPKGYHANFCLGCPPIWMSLDT 74

RESULT 2  
A40057  
transforming growth factor beta-1 precursor - bovine (fragment)  
N:Alternate names: beta-RGF; cartilage-inducing factor-A; EGF-dependent TGF or deGF; MGF  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 09-Jul-2004  
C:Accession: A40057; A42320; A05284; A24322; B61439  
R:Van Oberghehen-Schilling, B.; Kondalish, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.  
Mol. Endocrinol. 1, 693-698, 1987  
A:Title: Complementary deoxyribonucleic acid cloning of bovine transforming growth facto  
A:Reference number: A40057; MUID:91042552; PMID:3153459  
A:Accession: A40057  
A:Molecule type: mRNA  
A:Residues: 1-315 <VAN>  
A:Cross-references: UNIPROT:P18341; GB:M36271; NID:G163747; PIDN:AAA30778.1; PID:G163748  
R:Ogawa, Y.; Schmidt, D.K.; Daech, J.R.; Chang, R.J.; Glaeser, C.B.  
J. Biol. Chem. 267, 2325-2328, 1992  
A:Title: Purification and characterization of transforming growth factor-beta2.3 and -be  
A:Reference number: A42320; MUID:92129307; PMID:1733936  
A:Accession: A42320  
A:Molecule type: protein  
A:Residues: 204-209, 'X', 211-217 <OGA>  
R:Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan, Y.C.E.; Stei  
Biochemistry 22, 5692-5698, 1983  
A:Title: Purification and properties of a type beta transforming growth factor from bovi  
A:Reference number: A05284; MUID:84104793; PMID:6607069

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A:Accession: A05284
A:Molecule type: protein
A:Residues: 204-218 <ROB>
R:Sevedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti, A.; Sie
A:Title: Cartilage-inducing factor-A. Apparent identity to transforming growth factor-b
A:Reference number: A24322; MUID:86195954; PMID:3754555
A:Accession: A24322
A:Molecule type: protein
A:Residues: 204-233 <SEY>
R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
J. Protein Chem. 10, 565-575, 1991
A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta
A:Reference number: A61439; MUID:92189724; PMID:1799413
A:Accession: B61439
A:Molecule type: protein
A:Residues: 204-209, 'X', '211-217', 'XX', '220-232' <JIN>
C:Comment: This polypeptide is composed of two polypeptide chains cross-linked by disulf
C:Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogenic a
ion. Cells grown in monolayer do not respond in a similar manner to these growth factors
C:Superfamily: Inhibin
C:Keywords: glycoprotein; growth factor; heterodimer
F:204-315/Product: transforming growth factor beta-1 #status experimental <MAT>
F:7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 145; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 8,7e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 237 HEPKGYHANFCLGCPYIWSLDT 259

RESULT 3
WFM2
transforming growth factor beta-1 precursor [validated] - human
N:Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta
C:Species: Homo sapiens (man)
C>Date: 28-Feb-1986 #sequence revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: A27513; A01395; A22290; I59664; S53444
R:Derynck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.
Nucleic Acids Res. 15, 3188-3189, 1987
A:Title: Intron-exon structure of the human transforming growth factor-beta precursor g
A:Reference number: A27513; MUID:87174845; PMID:3470709
A:Accession: A27513
A:Molecule type: DNA
A:Residues: 1-390 <DER>
A:Cross-references: UNIPROT:P01137; GB:X05839; GB:Y00112; NID:G37097; PID:CAA29283.1; F
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assoian, R.K.; Robert
Nature 316, 701-705, 1985
A:Title: Human transforming growth factor-beta complementary DNA sequence and expression
A:Reference number: A01395; MUID:85296501; PMID:3861940
A:Accession: A01395
A:Molecule type: mRNA
A:Residues: 1-9, 'P', '11-24', 'P', '26-159', 'R', '160-390' <DER>
A:Cross-references: GB:X02812; GB:005114; NID:G37092; PID:CAA26580.1; PID:G37093
A>Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a
R:Massague, J.; Like, B.
J. Biol. Chem. 260, 2636-2645, 1985
A:Title: Cellular receptors for type beta transforming growth factor. Ligand binding and
A:Reference number: A22290; MUID:85131019; PMID:2982829
A:Accession: A22290
A:Molecule type: protein
A:Residues: 279-285, 'XX', '298-301' <MAS>
R:Urnishizaki, Y.; Nishizu, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.; Urushizaki,
Tumor Res. 22, 41-55, 1987
A:Title: Cloning and expression of the gene for human transforming growth factor-beta in
A:Reference number: I59664
A:Accession: I59664
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 279-390 <RES>

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A:Cross-references: GB:M38449; NID:G339557; PID:AAA36735.1; PID:G339558
R:Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyo, D.; Chait, B.T.; Marshak, D.R.,
Biochem. J. 305, 87-92, 1995
A:Title: Physical and biological characterization of a growth-inhibitory activity purified
A:Reference number: S53444; MUID:95126934; PMID:7826358
A:Accession: S53444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 279-297 <STA>
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
C:Genetics:
A:Gene: GDB:TGFB1, TGFB
A:Cross-references: GDB:120729; OMIM:190180
A:Map position: 19q13.2-19q13.2
C:Superfamily: Inhibin
C:Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation
F:11-18/Domain: signal sequence #status predicted <SIG>
F:19-278/Domain: propeptide #status predicted <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 145; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 312 HEPKGYHANFCLGCPYIWSLDT 334

RESULT 4
WMS2
transforming growth factor beta-1 precursor - mouse
N:Alternate names: TGF type 2; TGF-beta
C:Species: Mus musculus (house mouse)
C>Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A01396
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.
J. Biol. Chem. 261, 4377-4379, 1986
A:Title: The murine transforming growth factor-beta precursor.
A:Reference number: A01396; MUID:86168129; PMID:3007454
A:Accession: A01396
A:Molecule type: mRNA
A:Residues: 1-390 <DER>
A:Cross-references: UNIPROT:P04202; GB:M13177; NID:G201952; PID:AAA40423.1; PID:G201953
A>Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
C:Superfamily: Inhibin
C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen; transform
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-278/Domain: propeptide #status predicted <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 145; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 312 HEPKGYHANFCLGCPYIWSLDT 334

RESULT 5
A26960
transforming growth factor beta-1 precursor - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C>Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text_change 09-Jul-2004
C:Accession: A26960
R:Sharples, K.; Plowman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
DNA 6, 239-244, 1987

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A>Title: Cloning and sequence analysis of simian transforming growth factor-beta cDNA.  
 A:Reference number: A26960; MUID:87246074; PMID:3474130  
 A:Accession: A26960  
 A:Molecule type: mRNA  
 A:Residues: 1-390 <SHA>  
 A:Cross-references: UNIPROT:P09533; GB:M16658; NID:g176552; PIDN:AAA53569.1; PID:g176553  
 C:Superfamily: Inhibin  
 C:Keywords: growth factor  
 F:1-16/Domain: signal sequence  
 F:17-390/Product: transforming growth factor beta #status predicted <SIG>

Query Match 100.0%; Score 145; DB 2; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYWSLDT 23  
 DB 312 HEPKGYHANFCLGCPPIYWSLDT 334

## RESULT 6

transforming growth factor beta-1 - dog  
 C/Species: Canis lupus familiaris (dog)  
 C/Date: 13-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 09-Jul-2004  
 C/Accession: J04023  
 R:Manning, A.M.; Auchampach, J.A.; Drony, R.F.; Slightom, J.L.  
 Gene 155, 307-308, 1995

A>Title: Cloning of a canine cDNA homologous to the human transforming growth factor-beta  
 A:Reference number: J04023; MUID:95237630; PMID:7721110  
 A:Accession: J04023  
 A:Molecule type: mRNA

A:Residues: 1-390 <MAN>  
 A:Cross-references: UNIPROT:P54831; GB:L34956; NID:g516071; PIDN:AAA51458.1; PID:g516072  
 C/Comment: This factor plays a multifunctional role as a regulator of mammalian cell gro

C/Genetics:  
 A:Gene: tgf-beta1  
 C:Superfamily: inhibin

C:Keywords: growth factor  
 F:288-390/Product: transforming growth factor beta 1 #status predicted <MAT>

Query Match 100.0%; Score 145; DB 2; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYWSLDT 23  
 DB 312 HEPKGYHANFCLGCPPIYWSLDT 334

## RESULT 7

A27512  
 transforming growth factor beta-1 precursor - pig  
 N/Alternate names: TGF-beta

C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 09-Jul-2004  
 C/Accession: A27512; A26356; I46657  
 R:Derynck, R.; Rhee, L.

Nucleic Acids Res. 15, 3187, 1987  
 A>Title: Sequence of the porcine transforming growth factor-beta precursor.  
 A:Reference number: A27512; MUID:87174844; PMID:3470708

A:Accession: A27512  
 A:Molecule type: mRNA

A:Residues: 1-390 <DER>  
 A:Cross-references: UNIPROT:P07200

R:Chelifez, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Moie, J.E.; Lucas, R.;  
 Cell 48, 409-415, 1987  
 A>Title: The transforming growth factor-beta system, a complex pattern of cross-reactive  
 A:Reference number: A26356  
 A:Accession: A26356

A:Molecule type: protein  
 A:Residues: 279-322 <CHE>  
 R:Kondalath, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn, M.B.; Robert

J. Biol. Chem. 263, 18333-18337, 1988

A>Title: cDNA cloning of porcine transforming growth factor-beta 1 mRNAs. Evidence for a

A:Reference number: I46657; MUID:89054010; PMID:2461367  
 A:Accession: I46657

A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-390 <KON>

A:Cross-references: GB:M23703; NID:g755044; PIDN:AAA64616.1; PID:g755045  
 C:Genetics:  
 A:Gene: TGF-beta-1  
 C:Superfamily: inhibin  
 C:Keywords: growth factor

Query Match 100.0%; Score 145; DB 2; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYWSLDT 23  
 DB 312 HEPKGYHANFCLGCPPIYWSLDT 334

## RESULT 8

transforming growth factor beta-1 - sheep  
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C/Date: 19-Dec-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
 C/Accession: I46463; S45115  
 R:Woodall, C.J.; McLaren, L.J.; Watt, N.J.  
 Gene 150, 371-373, 1994

A>Title: Sequence and chromosomal localisation of the gene encoding ovine latent transfo  
 A:Reference number: I46463; MUID:95121932; PMID:7821809  
 A:Accession: I46463

A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA

A:Residues: 1-390 <MOO>  
 A:Cross-references: UNIPROT:P50414; EMBL:X76916; NID:g496648; PIDN:CAA54242.1; PID:g49666  
 A>Note: submitted to the EMBL Data Library, December 1993  
 C:Superfamily: inhibin

Query Match 100.0%; Score 145; DB 2; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYHANFCLGCPPIYWSLDT 23  
 DB 312 HEPKGYHANFCLGCPPIYWSLDT 334

## RESULT 9

S10219  
 transforming growth factor beta-1 precursor - rat  
 N/Alternate names: TGF type 2; TGF-beta

C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
 C/Accession: S10219; P70023; S02267  
 R:Qian, S.W.; Kondalath, P.; Roberts, A.B.; Sporn, M.B.

Nucleic Acids Res. 18, 3059, 1990  
 A>Title: cDNA cloning by PCR of rat transforming growth factor beta-1.  
 A:Reference number: S10219; MUID:90272425; PMID:2349108

A:Accession: S10219  
 A:Molecule type: mRNA

A:Residues: 1-390 <QIA>  
 A:Cross-references: UNIPROT:P17246; EMBL:X52498; NID:g57341; PIDN:CAA36741.1; PID:g57342  
 R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.

J. Biochem. 106, 304-310, 1989  
 A>Title: Purification and structural analysis of a latent form of transforming growth fa  
 A:Reference number: P70023; MUID:90036779; PMID:2478527

A:Accession: P70023  
 A:Molecule type: protein  
 A:Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 <OKA>  
 R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.  
 FEBS Lett. 242, 240-244, 1989

A>Title: One of two subunits of masking protein in latent TGF-beta is a part of pro-TGF-  
A:Reference number: S02267; MUID:89121078; PMID:2914605  
A:Accession: S02267  
A:Molecule type: protein  
A:Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 <OK>  
C:Superfamily: Inhibin  
C:Keywords: glycoprotein; growth factor; integrin binding  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-278/Domain: propeptide #status experimental <PRO>  
F:24-246/Region: cell attachment (R-G-D) motif  
F:29-390/Product: transforming growth factor beta-1 #status predicted <MAT>  
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 145; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 1.1e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYANFCLGCPYIWSLDT 23  
Db 312 HEPKGYANFCLGCPYIWSLDT 334

RESULT 10  
S01413  
transforming growth factor beta-1 precursor - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: S01413  
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.  
Nucleic Acids Res. 16, 8730, 1988  
A>Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1).  
A:Reference number: S01413; MUID:88335639; PMID:3166520  
A:Accession: S01413  
A:Molecule type: DNA  
A:Residues: 1-391 <JAK>  
A:Cross-references: UNIPROT:P07200; EMBL:X12373; NID:963808; PIDN:CAA30933.1; PID:963808  
C:Superfamily: Inhibin  
C:Keywords: growth factor

Query Match 100.0%; Score 145; DB 2; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.1e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEPKGYANFCLGCPYIWSLDT 23  
Db 313 HEPKGYANFCLGCPYIWSLDT 335

RESULT 11  
A41918  
transforming growth factor beta-4 precursor - chicken (fragment)  
N:Alternate names: TGF-beta 4  
C:Species: Gallus gallus (chicken)  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: A41918; A34941; S03110  
R:Butt, D.W.; Jakowlew, S.B.  
Mol. Endocrinol. 6, 989-992, 1992  
A>Title: Correction: a new interpretation of a chicken transforming growth factor-beta 4  
A:Reference number: A41918; MUID:92357039; PMID:1355860  
A:Accession: A41918  
A:Molecule type: mRNA  
A:Residues: 1-373 <BUR>  
A:Cross-references: UNIPROT:P09531; GB:M31160; GB:X08012; GB:S41706; NID:91262437; PIDN:  
A:Note: sequence extracted from NCBI backbone (NCBI:110106, NCBI:P:110187)  
A:Note: this report corrects and reinterprets the sequence from reference A34941  
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.  
Mol. Endocrinol. 2, 1186-1195, 1988  
A>Title: Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid end  
A:Accession: A34941; MUID:89112198; PMID:2464131  
A:Reference number: A34941  
A:Molecule type: mRNA  
A:Residues: 1-382 <KON>  
A:Cross-references: UNIPROT:P16176; GB:J05180; NID:9214821; PIDN:AAA49968.1; PID:9214822  
R:Roberts, A.B.; Rosa, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Rebbert, M.L.; Kondr  
A:Cross-references: EMBL:X08012

A>Note: this sequence has been corrected in A41918  
C:Superfamily: Inhibin  
C:Keywords: glycoprotein; growth factor  
F:1/Domain: signal sequence (fragment) #status predicted <SIG>  
F:223-225/Region: cell attachment (R-G-D) motif  
F:260-373/Product: transforming growth factor beta-4 #status predicted <MAT>  
F:54,109,153/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.3%; Score 128; DB 2; Length 373;  
Best Local Similarity 87.0%; Pred. No. 2.4e-10;  
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HEPKGYANFCLGCPYIWSLDT 23  
Db 295 HEPKGYANFCLGCPYIWSLDT 317

RESULT 12  
A39489  
transforming growth factor beta-2 precursor - chicken  
N:Alternate names: TGF-beta2  
C:Species: Gallus gallus (chicken)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C:Accession: A39489; A61018; S25849  
R:Butt, D.W.; Paton, I.R.  
DNA Cell Biol. 10, 723-734, 1991  
A>Title: Molecular cloning and primary structure of the chicken transforming growth factor  
A:Reference number: A39489; MUID:92075163; PMID:1683775  
A:Accession: A39489  
A:Molecule type: DNA  
A:Residues: 1-412 <BUR>  
A:Cross-references: UNIPROT:P30371; GB:X58071; NID:963810; PIDN:CAA41101.1; PID:9833616;  
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.  
Growth Factors 2, 123-133, 1990  
A>Title: Complementary deoxyribonucleic acid cloning of an mRNA encoding transforming gr  
A:Reference number: A61018; MUID:90253805; PMID:2340183  
A:Accession: A61018  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-94, 'G', 96-244, 'L', 246-412 <JAK>  
C:Genetics:  
A:Introns: 115/1, 169/3, 214/1, 251/1, 309/2, 360/3  
C:Superfamily: Inhibin  
C:Keywords: growth factor; growth regulation; mitogen; transformation  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-300/Domain: propeptide #status predicted <PRO>  
F:301-412/Product: transforming growth factor beta-2 #status predicted <MAT>

Query Match 85.5%; Score 124; DB 2; Length 412;  
Best Local Similarity 82.6%; Pred. No. 9.3e-10;  
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HEPKGYANFCLGCPYIWSLDT 23  
Db 334 HEPKGYANFCLGCPYIWSLDT 356

RESULT 13  
B61036  
transforming growth factor beta-5 precursor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 31-Dec-1993 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: A34929; B61036  
R:Kondratiah, P.; Sande, M.J.; Smith, J.M.; Fielde, A.; Roberts, A.B.; Sporn, M.B.; Melton,  
J. Biol. Chem. 265, 1089-1093, 1990  
A>Title: Identification of a novel transforming growth factor-beta (TGF-beta5) mRNA in X  
A:Reference number: A34929; MUID:90110090; PMID:2295601  
A:Accession: A34929  
A:Molecule type: mRNA  
A:Residues: 1-382 <KON>  
A:Cross-references: UNIPROT:P16176; GB:J05180; NID:9214821; PIDN:AAA49968.1; PID:9214822  
R:Roberts, A.B.; Rosa, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Rebbert, M.L.; Kondr  
Growth Factors 2, 135-147, 1990

A;Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium conditioned A;Reference number: A61036; MUID:90253806; PMID:2340184  
A;Accession: B61036  
A;Molecule type: protein  
A;Residues: 271-276, 'X', 278-284, 'XX', 287-299 <ROB>  
C;Superfamily: inhibin  
C;Keywords: growth factor  
F;271-382/Product: transforming growth factor beta-5 #status experimental <MAT>  
Query Match 84.8%; Score 123; DB 2; Length 382;  
Best Local Similarity 82.6%; Pred. No. 1.2e-09;  
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 HEPKGYHANFCLGCPYIWSLDT 23  
Db 304 HEPKGYHANFCLGNCPIYIWSMDT 326  
RESULT 14  
A61439  
transforming growth factor beta-2 - bovine  
N;Alternate names: cartilage-inducing factor B; MGF-a; milk growth factor a  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 07-Oct-1994 #sequence revision 07-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: A61439; A25485; B42320; S15389  
R;Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.  
J;Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta  
A;Reference number: A61439; MUID:92189724; PMID:1799413  
A;Accession: A61439  
A;Molecule type: protein  
A;Residues: 1-112 <JIN>  
A;Cross-references: UNIPROT:P21214  
A;Experimental source: milk  
R;Seyedin, S.M.; Segarini, P.R.; Rosen, D.M.; Thompson, A.Y.; Bentz, H.; Graycar, J.  
J; Biol. Chem. 262, 1946-1949, 1987  
A;Title: Cartilage-inducing factor-B is a unique protein structurally and functionally r  
A;Reference number: A25485; MUID:87137406; PMID:3469199  
A;Accession: A25485  
A;Molecule type: protein  
A;Residues: 1-30 <SEY>  
A;Experimental source: bone  
R;Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.U.; Glaser, C.B.  
J; Biol. Chem. 267, 2325-2328, 1992  
A;Title: Purification and characterization of transforming growth factor-beta2.3 and -be  
A;Reference number: A42320; MUID:92129307; PMID:1733936  
A;Accession: B42320  
A;Molecule type: protein  
A;Residues: 1-6, 'X', 8-14, 'XX', 17-34 <OGA>  
A;Experimental source: bone  
R;Cox, D.A.; Buerk, R.R.  
Eur. J. Biochem. 197, 353-358, 1991  
A;Title: Isolation and characterization of milk growth factor, a transforming-growth-fac  
A;Reference number: S15389; MUID:91224126; PMID:2026157  
A;Accession: S15389  
A;Molecule type: protein  
A;Residues: 1-16, 'XX', 19 <COX>  
A;Experimental source: milk  
C;Superfamily: inhibin  
C;Keywords: growth factor; growth regulation; heterodimer; homodimer  
Query Match 80.7%; Score 117; DB 2; Length 112;  
Best Local Similarity 78.3%; Pred. No. 2.7e-09;  
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 HEPKGYHANFCLGCPYIWSLDT 23  
Db 34 HEPKGYHANFCLGACPIYIWSMDT 56  
RESULT 15  
WPXLB2  
transforming growth factor beta-2 precursor - African clawed frog

C;Species: Xenopus laevis (African clawed frog)  
C;Date: 12-Feb-1993 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004  
C;Accession: S09510; A61036  
R;Rebert, M.L.; Bhattacharya, N.; David, I.B.  
Nucleic Acids Res. 18, 2185, 1990  
A;Title: The sequence of TGF-beta2 from Xenopus laevis.  
A;Reference number: S09510; MUID:90245678; PMID:2336403  
A;Accession: S09510  
A;Molecule type: mRNA  
A;Residues: 1-413 <REB>  
A;Cross-references: UNIPROT:P17247; EMBL:X51817; NID:9414789; PIDN:CA36116.1; PID:96513  
R;Roberts, A.B.; Rosa, F.; Roche, N.S.; Colligan, J.E.; Garfield, M.; Rebert, M.L.; Kond  
Growth Factors 2, 135-147, 1990  
A;Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium condition  
A;Reference number: A61036; MUID:90253806; PMID:2340184  
A;Accession: A61036  
A;Molecule type: protein  
A;Residues: 302-307, 'X', 309-315, 'XX', 318-319 <ROB>  
C;Superfamily: inhibin  
C;Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-301/Domain: propeptide #status predicted <PRO>  
F;302-413/Product: transforming growth factor beta-2 #status predicted <MAT>  
F;72,140,241/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 80.7%; Score 117; DB 1; Length 413;  
Best Local Similarity 78.3%; Pred. No. 8.8e-09;  
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 HEPKGYHANFCLGCPYIWSLDT 23  
Db 335 HEPKGYHANFCLGACPIYIWSMDT 357  
Search completed: June 14, 2005, 15:52:10  
Job time : 25.6538 secs

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## OM protein - protein search, using sw model

Run on: June 14, 2005, 15:34:23 ; Search time 122.962 Seconds  
(without alignments)  
95.785 Million cell updates/sec

Title: US-09-831-253F-10  
Perfect score: 145  
Sequence: 1 HEPKGYHANFCLGPCPYMSLDT 23

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:.\*  
1: uniprot\_sprotc:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	145	100.0	50 2 Q28240	Q28240 cervus elap
2	145	100.0	51 2 Q72487	Q72487 homo sapien
3	145	100.0	78 2 Q70316	Q70316 sus scrofa
4	145	100.0	112 2 Q02730	Q02730 oryctolagus
5	145	100.0	124 2 Q95N80	Q95N80 canis faml1
6	145	100.0	130 2 Q08714	Q08714 mesocricetu
7	145	100.0	315 1 TGFI_BOVIN	P18341 bos taurus
8	145	100.0	368 2 Q8R4D9	Q8R4D9 sigmodon hi
9	145	100.0	390 1 TGFI_CANPA	P54831 canis faml1
10	145	100.0	390 1 TGFI_CANPA	Q94196 cavia porce
11	145	100.0	390 1 TGFI_CERAE	P09533 cercopithec
12	145	100.0	390 1 TGFI_HORSE	O19011 equus cabal
13	145	100.0	390 1 TGFI_HUMAN	P01137 homo sapien
14	145	100.0	390 1 TGFI_MOUSE	P04202 mus musculu
15	145	100.0	390 1 TGFI_PIG	P07200 sus scrofa
16	145	100.0	390 1 TGFI_RAT	P17246 rattus norv
17	145	100.0	390 1 TGFI_SHEEP	P50414 ovib aries
18	145	100.0	390 2 Q9TUM6	Q9TUM6 equus cabal
19	138	95.2	101 2 Q9R184	Q9R184 meriones un
20	128	88.3	373 1 TGFI_CHICK	P09531 gallus galli
21	124	85.5	412 1 TGFI_CHICK	P30371 gallus galli
22	123	84.8	382 1 TGFI_XENLA	P16176 xenopus lae
23	118	81.4	77 2 Q90YF8	Q90YF8 oncorhynch
24	118	81.4	88 2 Q90YF7	Q90YF7 oncorhynch
25	118	81.4	91 2 Q9MYZ1	Q9MYZ1 capra hircu
26	118	81.4	361 2 Q98854	Q98854 cyprinus ca
27	118	81.4	410 2 Q66123	Q66123 brachydanio
28	118	81.4	410 2 Q7SZV3	Q7SZV3 brachydanio
29	118	81.4	411 2 Q90YF4	Q90YF4 pleuronecte
30	117	80.7	62 2 Q28241	Q28241 cervus elap
31	117	80.7	86 2 Q28241	Q28241 cervus elap

32	117	80.7	112 1 TGFI_BOVIN	P21214 bos taurus
33	117	80.7	224 2 Q8CDZ9	Q8CDZ9 mus musculu
34	117	80.7	255 2 Q921R1	Q921R1 mus musculu
35	117	80.7	399 2 Q9ERB7	Q9ERB7 mesocricetu
36	117	80.7	413 1 TGFI_XENLA	P17247 xenopus lae
37	117	80.7	414 1 TGFI_CERAE	P61811 cercopithec
38	117	80.7	414 1 TGFI_HUMAN	P61812 homo sapien
39	117	80.7	414 1 TGFI_MOUSE	P27090 mus musculu
40	117	80.7	414 2 Q91VP5	Q91VP5 mus musculu
41	117	80.7	435 1 TGFI_PIG	P09856 sus scrofa
42	117	80.7	442 1 TGFI_RAT	Q07257 rattus norv
43	117	80.7	442 2 Q6TFC3	Q6TFC3 oryctolagus
44	112	77.2	62 2 Q90YF9	Q90YF9 oncorhynch
45	112	77.2	62 2 Q90ZJ8	Q90ZJ8 anguilla an

## ALIGNMENTS

RESULT 1  
Q28240 PRELIMINARY; PRT; 50 AA.  
ID Q28240  
AC Q28240  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Transforming growth factor beta 1 (TGF-beta 1) (Transforming growth factor B1) (Fragment).  
GN Name=TGFBI; Synonyms=TGF beta-1, TGF-B1;  
OS Cervus elaphus (Red deer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae; OC Cervinae; Cervus.  
OX NCBI\_TaxID=96860;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Antler;  
RX MEDLINE=98233260; PubMed=9571767;  
RX DOI=10.1002/(SICI)1097-010X(19980501)281:1<36::AID-JEZ6>3.0.CO;2-D;  
RA Francis S.M., Suttie J.M.;  
RT "Detection of growth factors and proto-oncogene mRNA in the growing tip of red deer (Cervus elaphus) antler using reverse-transcriptase polymerase chain reaction (RT-PCR).";  
RL J. Exp. Zool. 281:36-42(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Wagener A., Bloctner S., Fickel J.;  
RT "Detection of growth factors in the testes of roe deer (Capreolus capreolus).";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.  
CC -!- SUBUNIT: Homodimer; disulfide-linked (by similarity).  
CC -!- SIMILARITY: Belongs to the TGF-beta family.  
DR EMBL; U62110; AAB05256.1; -.  
DR EMBL; AF152591; AAF73230.1; -.  
DR HSSP; P01137; IKLA.  
DR GO; GO:0008083; P:growth factor activity; IEA.  
DR GO; GO:0008283; P:cell proliferation; IEA.  
DR GO; GO:000074; P:regulation of cell cycle; IEA.  
DR InterPro; IPR001839; TGFb.  
DR Pfam; PF00019; TGF\_beta; 1.  
DR ProDom; PD000357; TGFb; 1.  
DR SMART; SMO0204; TGFb; 1.  
DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
KW Glycoprotein; Growth factor; Mitogen.  
FT NON\_TER  
FT CHAIN 1  
FT 1  
FT >50 TRANSFORMING GROWTH FACTOR BETA 1.

FT	NON TER	50	50	
SO	SEQUENCE	50 AA;	6012 MW;	ODDDAE48C640759F CRC64;
	Query Match		100.0%;	Score 145; DB 2; Length 50;
	Best Local Similarity		100.0%;	Pred. No. 1.5e-13;
	Matches	23; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
QY		1 HEPRGYHANFCIGRCPYIWSLDT	23	
Db		26 HEPRGYHANFCIGRCPYIWSLDT	48	

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RESULT 2
Q72487      PRELIMINARY;          PRT;          51 AA.
ID   Q72487
AC   Q72487;
DT   01-OCT-2003 (TREMBLrel. 25, Created)
DT   01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE   Transforming growth factor beta 1 (Fragment).
GN   Name=TFB1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Vieira A.R., Murray J.C.;
RA   Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC   -1- SIMILARITY: Belongs to the TGF-beta family.
DR   EMBL, AY330202; AAQ18642.1; -.
DR   HSBP; P01137; IKLA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   InterPro; IPR001839; TGPB.
DR   Pfam; PF00019; TGF_beta; 1.
DR   Prodom; PD000357; TGPB; 1.
DR   SMART; SM00204; TGFBI; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
DR   Growth factor.
FT   NON TER                    1
FT   NON TER                    1
FT   NON TER                    1
SQ   SEQUENCE      51 AA;  6140 MW;  259F4DB23E48A9D0 CRC64;
Query Match      100.0%; Score 145; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      1 HEPKGYHANFCLGPCPYIWSLDT 23
DB      25 HEPKGYHANFCLGPCPYIWSLDT 47

RESULT 3
Q70316      PRELIMINARY;          PRT;          78 AA.
ID   Q70316
AC   Q70316;
DT   05-JUL-2004 (TREMBLrel. 27, Created)
DT   05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE   Transforming growth factor beta 1 (Fragment).
GN   Name=TFB1;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kopecky M., Stratil A., Van Poucke M., Bartenschlager H.,
RA   Geldermann H., Peelman L.J.;
RA   Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC   -1- SIMILARITY: Belongs to the TGF-beta family.
DR   EMBL, AJ621785; CAF21862.1; -.
DR   HSBP; P01137; IKLA.

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DR	GO:0008083; F:growth factor activity; IEA.
DR	InterPro: IPR001839; TGFb.
DR	pfam; PF00019; TGF_beta; 1.
DR	ProDom; PD000357; TGFb; 1.
DR	SMART; SM00204; TGFb; 1.
DR	PROSITE; PS00250; TGF_BETA_1; 1.
KW	Growth factor.
FT	NON_TER 1 1
FT	CHAIN <1 >78 transforming growth factor beta 1.
FT	NON_TER 78 78
SO	SEQUENCE 78 AA; 8981 MW; 1BA179EL47738152 CRC64;
Qy	Query Match 100.0%; Score 145; DB 2; Length 78;
Db	Best Local Similarity 100.0%; Pred. No. 2,3e-13;
	Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 HEPKGYANFCLGPCPYIMSDT 23
	18 HEPKGYANFCLGPCPYIMSDT 40
RESULT 4	
ID	002730 PRELIMINARY; PRT; 112 AA.
AC	002730; 097501;
DT	01-JUL-1997 (TrEMBLrel. 04, Created)
DT	01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN	Name=TGFb1; Synonyms=TGF-beta-1;
OS	Oryctolagus cuniculus (Rabbit).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euteria; Lagomorpha; Leporidae; Oryctolagus.
OX	NCBI_TaxID=9986;
RA	SEQUENCE FROM N.A.
RA	Taylor T. K., James E. R., McGonigle S., Yoho E. R.;
RL	Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RL	(2)
RP	SEQUENCE OF 2-99 FROM N.A.
RA	Inoue K., Kawabe Y., Kodama T.;
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC	-1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC	-1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC	-1- SIMILARITY: Belongs to the TGF-beta family.
CC	EMBL; AF000133; AAB53806.1; -
DR	EMBL; AB020217; BAA36950.1; -
DR	HSSP; P0137; 1KLA.
DR	GO: GO:0008083; F:growth factor activity; IEA.
DR	GO: GO:0008283; P:cell proliferation; IEA.
DR	GO: GO:000074; P:regulation of cell cycle; IEA.
DR	InterPro: IPR002400; Gf_cysknob.
DR	InterPro: IPR001839; TGFb.
DR	pfam; PF00019; TGF_beta; 1.
DR	PRINTS; PR00438; GFCYSKNOT.
DR	ProDom; PD000357; TGFb; 1.
DR	SMART; SM00204; TGFb; 1.
DR	PROSITE; PS00250; TGF_BETA_1; 1.
KW	Glycoprotein; Growth factor; Mitogen.
FT	NON_TER 1 1
FT	CHAIN 1 112 TRANSFORMING GROWTH FACTOR BETA 1.
FT	DISULFID 7 16 BY SIMILARITY.
FT	DISULFID 15 78 BY SIMILARITY.
FT	DISULFID 44 109 BY SIMILARITY.
FT	DISULFID 48 111 BY SIMILARITY.
FT	DISULFID 77 77 INTERCHAIN (BY SIMILARITY).
FT	CONFLICT 2 3 ID -> FS (IN REF. 2).
FT	CONFLICT 85 92 PLEIYIV -> ATAHRTTIL (IN REF. 2).

RESULT 4			
002730	PRELIMINARY;	PRT;	112 AA.
ID 002730			
AC 002730;	097501;		
DT 01-JUL-1997	(TREMBLrel. 04, Created)		
DT 01-JUL-1997	(TREMBLrel. 04, Last sequence update)		
DT 01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	Transforming growth factor beta 1 (TGF-beta 1) (Fragment).		
GN	Name=TGFb1; Synonyms=TGF-beta-1;		
OS	Euryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
NCBI	taxid=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Taylor T.K., James E.R., McGonigle S., Yoho E.R.;		
RL	Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE OF 2-99 FROM N.A.		
RA	Inoue K., Kawabe Y., Kodama T.;		
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS		
CC	PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL		
CC	TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF		
CC	THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1		
CC	REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND		
CC	DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.		
CC	-1- SUBUNIT: Homodimer; disulfide-linked (By similarity).		
CC	-1- SIMILARITY: Belongs to the TGF-beta family.		
DR	EMBL; AF000133; AAB53806.1; -.		
DR	EMBL; AB020217; BAA36950.1; -.		
DR	HSSP; P0137; IKLA.		
DR	GO; GO:0008083; F: growth factor activity; IEA.		
DR	GO; GO:0008283; P: cell proliferation; IEA.		
DR	GO; GO:0000074; P: regulation of cell cycle; IEA.		
DR	InterPro; IPR002400; GF_cysknot.		
DR	InterPro; IPR001839; TGFb.		
DR	Pfam; PF00019; TGF_beta.1.		
DR	PRINTS; PR00438; GFCSKNOT.		
DR	Prodom; P000357; TGFb.1.		
DR	SMART; SM00204; TGFb.1.		
DR	PROSITE; PS00250; TGF_BETA_1; 1.		
KW	Glycoprotein; Growth factor; Mitogen.		
FT	NON TER	1	
FT	CHAIN	1	
FT	DISULFID	7	112 TRANSFORMING GROWTH FACTOR BETA 1.
FT	DISULFID	15	BY SIMILARITY.
FT	DISULFID	44	BY SIMILARITY.
FT	DISULFID	48	BY SIMILARITY.
FT	DISULFID	77	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	2	ID -> FS (IN REF. 2).
FT	CONFLICT	85	PLPIYIV -> ATAHRTTIL (IN REF. 2).

SQ SEQUENCE 112 AA; 12795 MW; 53C5B7D46355A6F3 CRC64;  
 Query Match 100.0%; Score 145; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-13;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HEPKGYHANFCLGCPYIWSLDT 23  
 |||||||  
 DB 34 HEPKGYHANFCLGCPYIWSLDT 56  
 |||||||  
 RESULT 5  
 Q95N80 PRELIMINARY; PRT; 124 AA.  
 ID Q95N80;  
 AC Q95N80;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE Transforming growth factor beta 1 (Fragment).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Fontana S., Groene A., Baumgaertner W.;  
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.  
 DR EMBL; AF349538; AAK54072.1; -.  
 DR HSSP; P01137; IKLA.  
 DR GO; GO:0008083; F:growth factor activity; IEA.  
 DR InterPro; IPR001839; TGFb.  
 DR Pfam; PF00019; TGF\_beta.1.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KM Growth factor.  
 FT NON\_TER 1 1  
 FT NON\_TER 124 124  
 SQ SEQUENCE 124 AA; 14329 MW; 21D185218E5556DB CRC64;  
 Query Match 100.0%; Score 145; DB 2; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-13;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HEPKGYHANFCLGCPYIWSLDT 23  
 |||||||  
 DB 49 HEPKGYHANFCLGCPYIWSLDT 71  
 |||||||  
 RESULT 6  
 Q08714 PRELIMINARY; PRT; 130 AA.  
 ID Q08714; 070331;  
 AC Q08714; 070331;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).  
 GN Name=TGFb1;  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=LVG (SVR);  
 RC MEDLINE=93304479; PubMed=8317544;  
 RX Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N.,  
 RA Elavic A., McBride J., Gallagher G., Todd R.;  
 RT "Sequential expression of transforming growth factors alpha and beta 1  
 RT by eosinophils during cutaneous wound healing in the hamster.";  
 RL Am. J. Pathol. 143:130-142(1993).

RN [2]  
 RP SEQUENCE OF 26-115 FROM N.A.  
 RC STRAIN=SYRIAN; TISSUE=SPLEEN;  
 RX MEDLINE=98234044; PubMed=9573100;  
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;  
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and  
 RT leishmaniasis.";  
 RT Infect. Immun. 66:2135-2142(1998).  
 RL -1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS  
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL  
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF  
 CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1  
 CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND  
 CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.  
 CC -1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED.  
 CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.  
 DR EMBL; X60296; CAA42838.1; -.  
 DR EMBL; AF046214; AAC40099.1; -.  
 DR PIR; I48196; I48196.  
 DR HSSP; P01137; IKLA.  
 DR GO; GO:0008083; F:growth factor activity; IEA.  
 DR GO; GO:0008283; P:cell proliferation; IEA.  
 DR GO; GO:0000704; P:regulation of cell cycle; IEA.  
 DR InterPro; IPR001839; TGFb.  
 DR Pfam; PF00019; TGF\_beta.1.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Glycoprotein; Growth factor; Mitogen.  
 FT NON\_TER 1 1  
 FT PROPEP <1 18  
 FT CHAIN 15 130  
 FT DISULFID 25 34  
 FT DISULFID 33 96  
 FT DISULFID 66 129  
 FT DISULFID 95 95  
 FT CONFLICT 93 93  
 SQ SEQUENCE 130 AA; 14997 MW; 8B41D6C39CCA77 CRC64;  
 Query Match 100.0%; Score 145; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-13;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HEPKGYHANFCLGCPYIWSLDT 23  
 |||||||  
 DB 52 HEPKGYHANFCLGCPYIWSLDT 74  
 |||||||  
 RESULT 7  
 TGF1\_BOVIN STANDARD; PRT; 315 AA.  
 ID TGF1\_BOVIN  
 AC P18341;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DE Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).  
 GN Name=TGFb1;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=91042552; PubMed=3153459;  
 RX van Obberghen-Schilling B., Kondalish P., Ludwig R.L., Sporn M.B.,  
 RA Baker C.C.;  
 RT "Complementary deoxyribonucleic acid cloning of bovine transforming  
 RT growth factor-beta 1.";  
 RL Mol. Endocrinol. 1:693-698(1987).  
 RL [2]  
 RP SUBUNITS.

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RC TISSUE=Bone;
RX MEDLINE=92129307; PubMed=1733936;
RA Ogawa Y., Schmidt D.K., Daesch J.R., Chang R.J., Glaser C.B.;
RT "Purification and characterization of transforming growth factor-beta
RT 2.3 and -beta 1.2 heterodimers from bovine bone.";
RL J. Biol. Chem. 267:2325-2328 (1992).
CC -1- FUNCTION: TGF-beta is a multifunctional peptide that controls
CC proliferation, differentiation, and other functions in many cell
CC types. Many cells synthesize TGF-beta and essentially all of them
CC have specific receptors for this peptide. TGF-beta regulates the
CC actions of many other peptide growth factors and determines a
CC positive or negative direction of their effects. Play an important
CC role in bone remodeling. It is a potent stimulator of
CC osteoblastic bone formation, causing chemotaxis, proliferation and
CC differentiation in committed osteoblasts (By similarity).
CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
CC covalently linked to a latency-associated peptide (LAP) homodimer.
CC The inactive complex can contain a latent TGF-beta binding protein
CC (By similarity). The active form is a homodimer of mature TGF-beta
CC 1; disulfide-linked. Heterodimers of TGF-beta 1/2 have been found
CC in bone.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
CC and LAP (By similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use. By non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M36271; AAA30778.1; -.
DR PIR; A40057; A40057.
DR HSSP; P01137; IKLA.
DR InterPro; IPR002400; GF_cyknok.
DR InterPro; IPR003911; TGF_TGFB.
DR InterPro; IPR001839; TGFB.
DR InterPro; IPR001111; TGFB_N.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein; Growth factor; Mitogen.
FT NON_TER 1
FT PROPEP 1
FT CHAIN 204 203 Transforming growth factor beta 1.
FT DISULFD 210 315 By similarity.
FT DISULFD 218 281 By similarity.
FT DISULFD 247 312 By similarity.
FT DISULFD 251 314 By similarity.
FT DISULFD 280 280 Interchain (By similarity).
FT CARBOHD 7 7 N-linked (GlcNAc...) (By similarity).
FT CARBOHD 61 61 N-linked (GlcNAc...) (By similarity).
FT CARBOHD 101 101 N-linked (GlcNAc...) (By similarity).
FT SITE 169 171 Cell attachment site (Potential).
SQ SEQUENCE 315 AA; 36269 MW; C2717A23D994800E CRC64;
Query Match 100.0%; Score 145; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 8.2e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HEPKGYHANFCLGCPPIYMSLDT 23
DB 237 HEPKGYHANFCLGCPPIYMSLDT 259

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OBRAD9 ID OBRAD9 PRELIMINARY; PRT; 368 AA.
AC OBRAD9;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Transforming growth factor beta-1 protein (Fragment).
GN Name=Tgfb1;
OS Sigmoidon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmoidon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14980081; DOI=10.1089/107999004772719873;
RA Bianco J.C., Pleneva L., Boukhalova M., Richardson J.Y.,
RA Harris K.A., Prince G.A.;
RT "The cotton rat: an underutilized animal model for human infectious
RT diseases can now be exploited using specific reagents to cytokines,
RT chemokines, and interferons."
RL J. Interferon Cytokine Res. 24:21-28(2004).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC EMBL; AF460858; AAB87199.1; -.
CC HSSP; P01137; IKLA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0005160; F:transforming growth factor beta receptor bi.; IEA.
DR GO; GO:0016049; P:cell growth; IEA.
DR InterPro; IPR002400; GF_cyknok.
DR InterPro; IPR001839; TGFB.
DR InterPro; IPR003939; TGFB.
DR InterPro; IPR001111; TGFB_N.
DR InterPro; IPR003911; TGF_TGFB.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR001423; TGFBETA.
DR PRINTS; PR01424; TGFBETA1.
DR PRODOM; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
FT NON_TER 1
SQ SEQUENCE 368 AA; 41905 MW; A5C91207B0468BA CRC64;
Query Match 100.0%; Score 145; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 9.4e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HEPKGYHANFCLGCPPIYMSLDT 23
DB 290 HEPKGYHANFCLGCPPIYMSLDT 312

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RESULT 9
ID TGF1_CANFA STANDARD; PRT; 390 AA.
AC P54831;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN Name=TGFBI;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue=Jugular vein endothelial;
RX MEDLINE=95237630; PubMed=7721110; DOI=10.1016/0378-1119(94)00903-6;
RX Manning A.W., Auchampach J.A., Drong R.F., Slightom J.L.;
RT "Cloning of a canine cDNA homologous to the human transforming growth

```



RT factor-beta 1-encoding gene.;  
RL Gene 155:307-308(1995).  
CC -1- FUNCTION: TGF-beta is a multifunctional peptide that controls  
CC proliferation, differentiation, and other functions in many cell  
CC types. Many cells synthesize TGF-beta and essentially all of them  
CC have specific receptors for this peptide. TGF-beta regulates the  
CC actions of many other peptide growth factors and determines a  
CC positive or negative direction of their effects. Play an important  
CC role in bone remodeling. It is a potent stimulator of  
CC osteoblastic bone formation, causing chemotaxis, proliferation and  
CC differentiation in committed osteoblasts (By similarity).  
CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
CC covalently linked to a latency-associated peptide (LAP) homodimer.  
CC The inactive complex can contain a latent TGF-beta binding  
CC protein. The active form is a homodimer of mature TGF-beta 1;  
CC disulfide-linked (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
CC and LAP (By similarity).  
CC -1- SIMILARITY: Belongs to the TGF-beta family.  
-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL: L34956; AAA51458.1; -;  
DR PIR: J04023; J04023.  
DR HSSP: P01137; IKLA.  
DR InterPro: IPR002400; GF\_cysknob.  
DR InterPro: IPR003911; TGF\_TGFB.  
DR InterPro: IPR001839; TGFB.  
DR InterPro: IPR001111; TGFB\_N.  
DR Pfam: PF00019; TGF\_beta; 1.  
DR Pfam: PF00688; TGFB\_propeptide; 1.  
DR PRINTS: PR00438; GRCYSKNOT.  
DR PRINTS: PR01423; TGFEBETA.  
DR PRODOM: PD000357; TGFB; 1.  
DR SMART: SM00204; TGFB; 1.  
DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
KM Glycoprotein: Growth Factor; Mitogen; Signal.  
FT SIGNAL 1 29 By similarity.  
FT PROPEP 30 278 Latency-associated peptide (By  
FT similarity).  
FT CHAIN 279 390 Transforming growth factor beta 1.  
FT DISULFID 285 294 By similarity.  
FT DISULFID 293 356 By similarity.  
FT DISULFID 322 387 By similarity.  
FT DISULFID 326 389 By similarity.  
FT CARBOHYD 355 355 Interchain.  
FT CARBOHYD 82 82 N-linked (GlcNAc...) (By similarity).  
FT CARBOHYD 136 136 N-linked (GlcNAc...) (By similarity).  
FT CARBOHYD 176 176 N-linked (GlcNAc...) (By similarity).  
FT SITE 244 246 Cell attachment site (Potential).  
SQ SEQUENCE 390 AA; 44185 MW; E84780E88B7B590E CRC64;  
Query Match 100.0%; Score 145; DB 1; Length 390;  
Best Local Similarity: 100.0%; Pred. No. 9,9e-13;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DR 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
GN Name=TGFBI;  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OC NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Hartley;  
RA Jeevan A., McMurray D.N., Yoshimura T.;  
RT "Guinea pig transforming growth factor-beta in peritoneal exudates  
RT after BCG vaccination.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 265-382 FROM N.A.  
RX MEDLINE=99144670; PubMed=10025978; DOI=10.1016/S1043-4666(98)90002-3;  
RA Scarozza A.M., Ramsingh A.I., Wicher V., Wicher K.;  
RT "Spontaneous cytokine gene expression in normal guinea pig blood and  
RT tissues";  
RL Cytokine 10:851-859(1998).  
RN [3]  
RP SEQUENCE OF 279-371 FROM N.A.  
RC STRAIN=Hartley; TISSUE=Trachea;  
RA Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,  
RA Sekizawa K.;  
RT "Guinea-pig transforming growth factor-beta expression in injured  
RT tracheal epithelium.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Multifunctional peptide that controls proliferation,  
CC differentiation, and other functions in many cell types. Many  
CC cells synthesize TGF-beta 1 and essentially all of them have  
CC specific receptors for this peptide. TGF-beta 1 regulates the  
CC actions of many other peptide growth factors and determines a  
CC positive or negative direction of their effects. Play an important  
CC role in bone remodeling. It is a potent stimulator of  
CC osteoblastic bone formation, causing chemotaxis, proliferation and  
CC differentiation in committed osteoblasts (By similarity).  
CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
CC covalently linked to a latency-associated peptide (LAP) homodimer.  
CC The inactive complex can contain a latent TGF-beta binding  
CC protein. The active form is a homodimer of mature TGF-beta 1;  
CC disulfide-linked (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
CC and LAP (By similarity).  
CC -1- SIMILARITY: Belongs to the TGF-beta family.  
-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL: AF191297; AF02780.1; -;  
DR EMBL: AF097509; AAC83807.1; -;  
DR EMBL: AF169347; AAD49347.1; -;  
DR HSSP: P01137; IKLA.  
DR InterPro: IPR002400; GF\_cysknob.  
DR InterPro: IPR003911; TGF\_TGFB.  
DR InterPro: IPR001839; TGFB.  
DR InterPro: IPR001111; TGFB\_N.  
DR Pfam: PF00019; TGF\_beta; 1.  
DR Pfam: PF00688; TGFB\_propeptide; 1.  
DR PRINTS: PR00438; GRCYSKNOT.  
DR PRINTS: PR01423; TGFEBETA.  
DR PRODOM: PD000357; TGFB; 1.  
DR SMART: SM00204; TGFB; 1.  
DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
KM Glycoprotein: Growth Factor; Mitogen; Signal.

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FT SIGNAL 1 29 By similarity.
FT PROPEP 30 278 latency-associated peptide (By
FT CHAIN 279 390 transforming growth factor beta 1.
FT DISULFID 285 294 By similarity.
FT DISULFID 293 356 By similarity.
FT DISULFID 322 387 By similarity.
FT DISULFID 326 389 By similarity.
FT CARBOHYD 355 355 Interchain (By similarity).
FT CARBOHYD 82 82 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 136 136 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 176 176 N-linked (GlcNAc...) (By similarity).
FT SITE 244 246 Cell attachment site (Potential).
FT CONFLICT 279 279 G -> P (in Ref. 3).
FT CONFLICT 286 286 F -> S (in Ref. 2).
FT CONFLICT 309 309 K -> R (in Ref. 2).
FT CONFLICT 322 322 C -> R (in Ref. 2).
FT CONFLICT 350 350 A -> G (in Ref. 2).
SQ SEQUENCE 390 AA; 44328 MW; 1539F849BA0C0CF1 CRC64;

Query Match 100.0%; Score 145; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 9.9e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 312 HEPKGYHANFCLGCPYIWSLDT 334

RESULT 11
TGFL_CERAE STANDARD; PRT; 390 AA.
ID TGFL_CERAE STANDARD; PRT; 390 AA.
AC P09533;
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN Name=TFB1;
OS Cercopithecus aethiops (Green monkey) (Primate).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87246074; PubMed=3474130;
RA Sharples K., Plowman G.D., Rose T.M., Twardzik D.R., Purchio A.F.;
RT "Cloning and sequence analysis of simian transforming growth factor-
beta cDNA."
RL DNA 6:239-244 (1987).
RN [2]
RP GLYCOSYLATION.
RX PubMed=2971654;
RA Purchio A.F., Cooper J.A., Brunner A.M., Lioubin M.N., Gentry L.E.,
RA Kovachina K.S., Roth R.A., Marguardt H.;
RT "Identification of mannose 6-phosphate in two asparagine-linked sugar
chains of recombinant transforming growth factor-beta 1 precursor."
RL J. Biol. Chem. 263:14211-14215 (1988).
RN [3]
RP CHARACTERIZATION.
RX PubMed=3185545;
RA Gentry L.E., Lioubin M.N., Purchio A.F., Marguardt H.;
RT "Molecular events in the processing of recombinant type 1 pre-pro-
transforming growth factor beta to the mature polypeptide."
RL Mol. Cell. Biol. 8:4162-4168 (1988).
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN Name=TFB1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.

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CC differentiation in committed osteoblasts (By similarity).
CC -1 SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-
CC covalently linked to a latency-associated peptide (LAP) homodimer.
CC The inactive complex can contain a latent TGF-beta binding
CC protein. The active form is a homodimer of mature TGF-beta 1;
CC disulfide-linked.
CC -1 SUBCELLULAR LOCATION: Secreted.
CC -1 PM: Glycosylated. The precursor is cleaved into mature TGF-beta 1
CC and LAP, which remains non-covalently linked to mature TGF-beta 1
CC rendering it inactive.
CC -1 SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; M16658; AAA5369.1; -.
DR PIR; A26960; A26960.
DR HSSP; P01137; 1KLA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR003911; TGF_TGFB.
DR InterPro; IPR001839; TGFB.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF00019; TGF_beta_1.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GRCYSKNOT.
DR PRINTS; PR01423; TGFbeta.
DR ProDom; PD000357; TGFb.1.
DR SMART; SM00204; TGFB.1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR GlycoProtein; Growth Factor; Mitogen; Signal.
KW SIGNAL
FT SIGNAL 1 29
FT PROPEP 30 278 latency-associated peptide.
FT CHAIN 279 390 Transforming growth factor beta 1.
FT DISULFID 285 294 By similarity.
FT DISULFID 293 356 By similarity.
FT DISULFID 322 387 By similarity.
FT DISULFID 326 389 By similarity.
FT DISULFID 355 355 Interchain (By similarity).
FT CARBOHYD 82 82 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 136 136 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 176 176 N-linked (GlcNAc...) (By similarity).
FT SITE 244 246 Cell attachment site (Potential).
SQ SEQUENCE 390 AA; 44356 MW; DFF63B2BBA44320B CRC64;

Query Match 100.0%; Score 145; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 9.9e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HEPKGYHANFCLGCPYIWSLDT 23
Db 312 HEPKGYHANFCLGCPYIWSLDT 334

RESULT 12
TGFL_HORSE STANDARD; PRT; 390 AA.
ID TGFL_HORSE STANDARD; PRT; 390 AA.
AC O19011;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN Name=TFB1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.

```

CC TISSUE=Lymph node;  
 RX MEDLINE=98185507; PubMed=9524819;  
 RA Penha-Goncalves M.N., Onions D.E., Nicolson L.;  
 RT "Cloning and sequencing of equine transforming growth factor-beta 1  
 (TGF-beta-1) cDNA.";  
 RL DNA Seq. 7:375-378(1997).  
 CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control  
 proliferation, differentiation, and other functions in many cell  
 types. Many cells synthesize TGF-beta and essentially all of them  
 have specific receptors for this peptide. TGF-beta regulates the  
 actions of many other peptide growth factors and determines  
 positive or negative direction of their effects. Play an important  
 role in bone remodelling. It is a potent stimulator of  
 osteoblastic bone formation, causing chemotaxis, proliferation and  
 differentiation in committed osteoblasts (By similarity).  
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
 covalently linked to a latency-associated peptide (LAP) homodimer.  
 CC The inactive complex can contain a latent TGF-beta binding  
 protein. The active form is a homodimer of mature TGF-beta 1;  
 CC disulfide-linked (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
 and LAP (By similarity).  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.  
 CC -----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; X99438; CA67801.1; -;  
 DR HSSP; P01137; 1KLA.  
 DR InterPro; IPR002400; GF\_cyskn0t.  
 DR InterPro; IPR003911; TGF\_TGFB.  
 DR InterPro; IPR001839; TGFB.  
 DR InterPro; IPR001111; TGFB\_N.  
 DR Pfam; PF00019; TGF\_Beta; 1.  
 DR Pfam; PF00688; TGFB\_propeptide; 1.  
 DR PRINTS; PR00438; GFCYSKN0T.  
 DR PRINTS; PR01423; TGFBEA.  
 DR PRODOM; PD000357; TGFB; 1.  
 DR SMART; SM00204; TGFB; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Glycoprotein; Growth factor; Mitogen; Signal.  
 FT SIGNAL 1 29  
 FT PROPEP 30 278  
 FT PROPEP 30 278  
 FT CHAIN 279 390  
 FT DISULFID 285 294  
 FT DISULFID 293 356  
 FT DISULFID 322 387  
 FT DISULFID 326 389  
 FT DISULFID 355 355  
 FT CARBOHYD 82 82  
 FT CARBOHYD 136 136  
 FT CARBOHYD 176 176  
 SQ SEQUENCE 390 AA; 43974 MW; A86D715F44549691 CRC64;  
 Query Match 100.0%; Score 145; DB 1; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-13;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC P01137; Q9UCG4;  
 DT 21-UTL-1986 (Rel. 01, Created)  
 DT 01-PEB-1991 (Rel. 17, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
 GN Name=TGFBI; Synonyms=TGFB;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87174845; PubMed=3470709;  
 RA Derynck R., Rhee L., Chen E.Y., van Tilburg A.;  
 RT "Intron-exon structure of the human transforming growth factor-beta  
 precursor gene.";  
 RL Nucleic Acids Res. 15:3188-3189(1987).  
 RN (2)  
 RP SEQUENCE FROM N.A., AND VARIANT PRO-10.  
 RX MEDLINE=85296301; PubMed=3861940;  
 RA Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,  
 RA Asseoli R.K., Roberts A.B., Sporn W.B., Goeddel D.V.;  
 RT "Human transforming growth factor-beta complementary DNA sequence and  
 expression in normal and transformed cells.";  
 RL Nature 316:701-705(1985).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ductum, and Eye;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Struhsberg R.L., Fehlgold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marutina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriques S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalske U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN (4)  
 RP SEQUENCE OF 279-390 FROM N.A.  
 RC TISSUE=Carcinoma;  
 RA Urushizaki Y., Terui T., Koshida Y., Mahara K., Kohgo Y.,  
 RA Urushizaki I., Takahashi Y., Ito H.;  
 RT "Cloning and expression of the gene for human transforming growth  
 factor-beta in Escherichia coli.";  
 RL Tumor Res. 22:41-55(1987).  
 RN (5)  
 RP SEQUENCE OF 279-329.  
 RC TISSUE=Bladder carcinoma;  
 RX MEDLINE=93229900; PubMed=8471846; DOI=10.1006/prep.1993.1019;  
 RA Bourdrel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugarman B.J.,  
 RA Hu S., Westcott K.R.;  
 RT "Recombinant human transforming growth factor-beta 1: expression by  
 Chinese hamster ovary cells, isolation, and characterization.";  
 RL Protein Expr. Purif. 4:130-140(1993).  
 RN (6)  
 RP SEQUENCE OF 279-301.  
 RX MEDLINE=85131019; PubMed=2982829;  
 RA Massague J., Like B.;  
 RT "Cellular receptors for type beta transforming growth factor. Ligand  
 binding and affinity labeling in human and rodent cell lines.";  
 RL J. Biol. Chem. 260:2636-2645(1985).

[7]  
 RP SEQUENCE OF 30-42 AND 279-290, AND CHARACTERIZATION.  
 RX PubMed=3162913;  
 RA Miyazono K., Hellman U., Wernstedt C., Heldin C.H.;  
 RT "Latent high molecular weight complex of transforming growth factor  
 RT beta 1. Purification from human platelets and structural  
 RT characterization.";  
 RL J. Biol. Chem. 263:6407-6415(1988).  
 RN [8]  
 RP REVIEW.  
 RX PubMed=9150447;  
 RA Munger J.S., Harpel J.G., Gleizes P.E., Mazzieri R., Nunes I.,  
 RA Rifkin D.B.;  
 RT "Latent transforming growth factor-beta: structural features and  
 RT mechanisms of activation.";  
 RL Kidney Int. 51:1376-1382(1997).  
 RN [9]  
 RP STRUCTURE BY NMR OF 279-390.  
 RX MEDLINE=93144319; PubMed=8424942;  
 RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,  
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,  
 RA Torchia D.A.;  
 RT "Transforming growth factor beta 1: NMR signal assignments of the  
 RT recombinant protein expressed and isotopically enriched using Chinese  
 RT hamster ovary cells.";  
 RL Biochemistry 32:1152-1163(1993).  
 RN [10]  
 RP STRUCTURE BY NMR OF 279-390.  
 RX MEDLINE=93144320; PubMed=8424943;  
 RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,  
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,  
 RA Torchia D.A.;  
 RT "Transforming growth factor beta 1: secondary structure as determined  
 RT by heteronuclear magnetic resonance spectroscopy.";  
 RL Biochemistry 32:1164-1171(1993).  
 RN [11]  
 RP STRUCTURE BY NMR OF 279-390.  
 RX MEDLINE=96266150; PubMed=8679613; DOI=10.1021/bi9604946;  
 RA Hinck A.P., Archer S.J., Qian S.W., Roberts A.B., Sporn M.B.,  
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,  
 RA Torchia D.A.;  
 RT "Transforming growth factor beta 1: three-dimensional structure in  
 RT solution and comparison with the X-ray structure of transforming  
 RT growth factor beta 2.";  
 RL Biochemistry 35:8517-8534(1996).  
 RN [12]  
 RP TISSUE SPECIFICITY.  
 RX PubMed=11746498; DOI=10.1002/jcb.1249;  
 RA Shur I., Lokiec F., Bleiberg I., Benayahu D.;  
 RT "Differential gene expression of cultured human osteoblasts.";  
 RL J. Cell. Biochem. 83:547-553(2001).  
 RN [13]  
 RP VARIANT PRO-10.  
 RX PubMed=9783545;  
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 RA Hase M., Takai H., Harada A., Ikeda K.;  
 RT "Association of a polymorphism of the transforming growth factor-beta1  
 RT gene with genetic susceptibility to osteoporosis in postmenopausal  
 RT Japanese women.";  
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 RN [14]  
 RP VARIANTS CED CVS-218; HIS-218 AND ARG-225.  
 RX PubMed=10973241; DOI=10.1038/79128;  
 RA Kinoshita A., Saito T., Tomita H., Makita Y., Yoshida K., Ghadami M.,  
 RA Yamada K., Kondo S., Ikegawa S., Nishimura G., Fukushima Y.,  
 RA Nakagomi T., Saito H., Sugimoto T., Kamegaya M., Hise K., Murray J.C.,  
 RA Taniguchi N., Nishikawa N., Yoshiura K.;  
 RT "Domain-specific mutations in TGFBI result in Camurati-Engelmann  
 RT disease.";  
 RL Nat. Genet. 26:19-20(2000).  
 RN [15]  
 RP VARIANTS CED HIS-81; CVS-218 AND ARG-225.  
 RX PubMed=11062463; DOI=10.1038/81563;

RA Janssens K., Gershon-Baruch R., Guanabens N., Mgone N., Ralston S.,  
 RA Bonduelle M., Lissens W., Van Maldergem L., Vanhoenacker F.,  
 RA Verbruggen L., Van Hul W.;  
 RT "Mutations in the gene encoding the latency-associated peptide of TGF-  
 RT beta 1 cause Camurati-Engelmann disease.";  
 RL Nat. Genet. 26:273-275(2000).  
 RN [16]  
 RP VARIANT PRO-10.  
 RX PubMed=12202987; DOI=10.1007/s100380200069;  
 RA Matanabe Y., Kinoshita A., Yamada T., Ohta T., Kishino T.,  
 RA Matsumoto N., Ishikawa M., Nishikawa N., Yoshiura K.;  
 RT "A catalog of 106 single-nucleotide polymorphisms (SNPs) and 11 other  
 RT types of variations in genes for transforming growth factor-beta1  
 RT (TGF-beta1) and its signaling pathway.";  
 RL J. Hum. Genet. 47:478-483(2002).  
 RN [17]  
 RP CHARACTERIZATION OF VARIANTS CED HIS-81; CVS-218; ASP-222 AND ARG-225.  
 RX PubMed=12493741; DOI=10.1074/jbc.M208857200;  
 RA Janssens K., ten Dijke P., Ralston S.H., Bergmann C., Van Hul W.;  
 RT "Transforming growth factor-beta-1 mutations in Camurati-Engelmann  
 RT disease lead to increased signaling by altering either activation or  
 RT secretion of the mutant protein.";  
 RL J. Biol. Chem. 278:7718-7724(2003).  
 RN [18]  
 RP CHARACTERIZATION OF VARIANT CVS-218.  
 RX PubMed=12843182; DOI=10.1210/jc.2002-020564;  
 RA McGowan N.W., Macpherson H., Janssens K., Van Hul W., Frith J.C.,  
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 RT "A mutation affecting the latency-associated peptide of TGFbeta1 in  
 RT Camurati-Engelmann disease enhances osteoclast formation in vitro.";  
 RL J. Clin. Endocrinol. Metab. 86:3521-3526(2003).  
 CC -1- FUNCTION: Multifunctional peptide that controls proliferation,  
 CC differentiation, and other functions in many cell types. Many  
 CC cells synthesize TGF-beta 1 and essentially all of them have  
 CC specific receptors for this peptide. TGF-beta 1 regulates the  
 CC actions of many other peptide growth factors and determines a  
 CC positive or negative direction of their effects. Play an important  
 CC role in bone remodeling. It is a potent stimulator of  
 CC osteoblastic bone formation, causing chemotaxis, proliferation and  
 CC differentiation in committed osteoblasts (By similarity).  
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
 CC covalently linked to a latency-associated peptide (LAP) homodimer.  
 CC The inactive complex can contain a latent TGF-beta binding  
 CC protein. The active form is a homodimer of mature TGF-beta 1;  
 CC disulfide-linked.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in bone.  
 CC -1- INDUCTION: Activated in vitro at pH below 3.5 and over 12.5.  
 CC -1- PTM: Glycosylated (By similarity). The precursor is cleaved into  
 CC mature TGF-beta 1 and LAP.  
 CC -1- POLYMORPHISM: In post-menopausal Japanese women, the frequency of  
 CC Leu-10 is higher in subjects with osteoporosis than in controls.  
 CC -1- DISEASE: Defects in TGFBI are the cause of Camurati-Engelmann

Query Match 100.0%; Score 145; DB 1; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 9,9e-13;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 HEPKGYHANFCLGCPYIWSLDT 23  
 Db 312 HEPKGYHANFCLGCPYIWSLDT 334

RESULT 14  
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 AC P04202;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 20-MAR-1987 (Rel. 04, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
 GN Name=Tgfb1;  
 OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=86168129; PubMed=3007454;  
 CC Derynck R., Jarrett J.A., Chen E.Y., Goeddel D.V.;  
 CC "The murine transforming growth factor-beta precursor.";  
 CC J. Biol. Chem. 261:4377-4379(1986).  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=BA16/C;  
 CC MEDLINE=96096545; PubMed=8522200; DOI=10.1016/0378-1119(95)00460-N;  
 CC Guron C., Sudarshan C., Raghow R.;  
 CC "Molecular organization of the gene encoding murine transforming  
 CC growth factor beta 1.";  
 CC J. Biol. Chem. 268:16532-16536(1993).  
 CC [3]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=C57BL/6, and NOB/LT; TISSUE=Spleen;  
 CC Polrot L., Benoist C., Mathis D.;  
 CC "Transforming growth factor-beta 1 sequence and expression: no  
 CC difference between NOD/Lt and C57BL/6 mouse strains.";  
 CC Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.  
 CC [4]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=FVB/N; TISSUE=Mammary gland;  
 CC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 CC Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 CC Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,  
 CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 CC Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 CC Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 CC Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 CC Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 CC Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 CC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 CC Fahey J., Helton E., Kettelman M., Madan A., Rodríguez S., Sanchez A.,  
 CC Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 CC Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 CC Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 CC Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 CC Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 CC "Generation and initial analysis of more than 15,000 full-length human  
 CC and mouse cDNA sequences.";  
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: TGF-beta is a multifunctional peptide that control  
 CC proliferation, differentiation, and other functions in many cell  
 CC types. Many cells synthesize TGF-beta and essentially all of them  
 CC have specific receptors for this peptide. TGF-beta regulates the  
 CC actions of many other peptide growth factors and determines a  
 CC positive or negative direction of their effects. Play an important  
 CC role in bone remodelling. It is a potent stimulator of  
 CC osteoblastic bone formation, causing chemotaxis, proliferation and  
 CC differentiation in committed osteoblasts (by similarity).  
 CC -1- SUBUNIT: The inactive form consists of a TGF-beta 1 homodimer non-  
 CC covalently linked to a latency-associated peptide (LAP) homodimer.  
 CC The inactive complex can contain a latent TGF-beta binding  
 CC protein. The active form is a homodimer of mature TGF-beta 1;  
 CC disulfide-linked (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: Glycosylated. The precursor is cleaved into mature TGF-beta 1  
 CC and LAP (by similarity).  
 CC -1- SIMILARITY: Belongs to the TGF-beta family.  
 CC -----  
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 CC DR EMBL; L42462; AAB00138.1; -;  
 CC DR EMBL; L42456; AAB00138.1; JOINED.  
 CC DR EMBL; L42457; AAB00138.1; JOINED.  
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 CC DR EMBL; L42459; AAB00138.1; JOINED.  
 CC DR EMBL; L42460; AAB00138.1; JOINED.  
 CC DR EMBL; L42461; AAB00138.1; JOINED.  
 CC DR EMBL; AJ009862; CA08900.1; -;  
 CC DR EMBL; BC013738; AAH13738.1; -;  
 CC DR PIR; A01396; WPM52.  
 CC DR HSSP; P01137; 1KLA.  
 CC DR MSP; MG198725; Tgfb1.  
 CC DR GO; GO:0005578; C:extracellular matrix; IDA.  
 CC DR GO; GO:0006954; P:inflammatory response; IMP.  
 CC DR GO; GO:0007515; P:lymph gland development; IMP.  
 CC DR GO; GO:0008220; P:necrosis; IMP.  
 CC DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.  
 CC DR GO; GO:0042127; P:regulation of cell proliferation; IDA.  
 CC DR GO; GO:0016202; P:regulation of myogenesis; IDA.  
 CC DR GO; GO:0042306; P:regulation of protein-nucleus import; IDA.  
 CC DR GO; GO:0007179; P:transforming growth factor beta receptor si. .; IDA.  
 CC DR InterPro; IPR002400; GF\_cyknct.  
 CC DR InterPro; IPR003911; TGF\_TGFB.  
 CC DR InterPro; IPR001839; TGFB.  
 CC DR InterPro; IPR001111; TGFB\_N.  
 CC DR Pfam; PF00019; TGF\_beta\_1.  
 CC DR Pfam; PF00688; TGF\_beta\_propeptide; 1.  
 CC DR PRINTS; PR00438; GFCYSKNOT.  
 CC DR PRINTS; PR01423; TGFBETA.  
 CC DR ProDom; PD000357; TGFB.  
 CC DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 CC DR GlycoProtein; Growth factor; Mitogen; Signal.  
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 CC FT CHAIN 279 390  
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 CC FT DISULFID 293 356  
 CC FT DISULFID 322 387  
 CC FT DISULFID 326 389  
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 CC FT CARBOHYD 82 82  
 CC FT CARBOHYD 136 136  
 CC FT CARBOHYD 176 176  
 CC FT SITE 244 246  
 CC SQ SEQUENCE 390 AA; 44310 MW; 4381A51B71ID689E CQC64;  
 CC Query Match 100.0%; Score 145; DB 13; Length 390;  
 CC Best local similarity 100.0%; Pred. No. 9.9e-13;  
 CC Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC Oy 1 HEPKGYHANFCLGCPYIWSIDT 23  
 CC Db 312 HEPKGYHANFCLGCPYIWSIDT 334  
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 CC RESULT 15  
 CC ID TGF1\_PIG STANDARD; PRT; 390 AA.  
 CC AC P07200; P08832;  
 CC DT 01-APR-1988 (Rel. 07, Created)  
 CC DT 01-APR-1988 (Rel. 07, Last sequence update)  
 CC DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 CC DE Transforming growth factor beta 1 precursor (TGF-beta 1).  
 CC GN Name=TGFBI;  
 CC OS Sus scrofa (Pig).  
 CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
 CC CC NCBI\_TaxID=9623;  
 CC CC [1]  
 CC CC SEQUENCE FROM N.A.

